```
OM of: US-09-623-304A-1 to: EST:*   out_format : pfs

Date: Aug 21, 2002  9:40 PM

About: Results were produced by the GenCore software, version 4.5,
       Copyright (c) 1993-2000 Compugen Ltd.

Command line parameters:
 -MODEL=frame+_p2n.model -DEV=xlh
 -Q=/cgn2_1/USPTO_spool/US09623304/runat_19082002_155554_23745/app_query.fasta_1.447
 -DB=EST -QFMT=fastap -SUFFIX=p2n.rst -GAPOP=12.000 -GAPEXT=4.000
 -MINMATCH=0.100 -LOOPCL=0.000 -LOOPEXT=0.000 -QGAPOP=4.500
 -QGAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500 -FGAPOP=6.000
 -FGAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500 -DELOP=6.000
 -DELEXT=7.000 -START=1 -MATRIX=blosum62 -TRANS=human40.cdi
 -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0
 -ALIGN=15 -MODE=LOCAL -OUTFMT=pfs -NORM=ext -HEAPSIZE=500
 -MINLEN=0 -MAXLEN=2000000000 -USER=US09623304_@CGN1_1_2744
 -NCPU=6 -ICPU=3 -LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30
 -NO_XLPXY -WAIT -THREADS=1

Search information block:
Query: US-09-623-304A-1
Query length: 383
Database: EST:*
Database sequences: 13736207
Database length: -1841457050
Search time (sec): 1594.010000


score_list:
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Sequence	Strd	Orig	ZScore	EScore	Len	! Documentation ..
gb_est2:BI143740	+	1272.00	2595.41	2.6e-135	858	! BI143740 602907395F1 NCI_CGAP_K
gb_est2:BI144257	+	1118.00	2279.06	1.1e-117	781	! BI144257 602907822F1 NCI_CGAP_K
gb_est2:BI143982	+	979.00	1992.93	9.2e-102	753	! BI143982 602908077F1 NCI_CGAP_K
gb_est2:BI101237	+	972.50	1981.11	4.2e-101	662	! BI101237 602886939F1 NCI_CGAP_K
gb_est2:BI101492	+	934.00	1901.30	1.2e-96	686	! BI101492 602887284F1 NCI_CGAP_K
gb_est2:BF780854	+	916.50	1864.80	1.3e-94	710	! BF780854 602105743F1 NCI_CGAP_K
gb_est2:BF789666	+	896.50	1822.37	2.9e-92	783	! BF789666 602105281F1 NCI_CGAP_K
gb_est2:BF411612	-	830.00	1690.36	6.6e-85	516	! BF411612 UI-R-BT1-bmp-d-10-0-UI
gb_est1:BB625105	+	810.00	1646.16	1.9e-82	658	! BB625105 BB625105 RIKEN full-le
gb_htc:AK017299	+	807.00	1623.85	3.3e-81	2462	! AK017299 Mus musculus 6 days n
gb_est2:BF789809	+	792.50	1609.95	2.0e-80	665	! BF789809 602105362F1 NCI_CGAP_K
gb_est1:BB643863	+	760.00	1543.39	1.0e-76	641	! BB643863 BB643863 RIKEN full-le
gb_est1:AW475637	+	752.50	1526.49	8.8e-76	721	! AW475637 un69d09.y1 Sugano mous
gb_est1:BB644922	+	744.00	1510.22	7.1e-75	651	! BB644922 BB644922 RIKEN full-le
gb_est2:BI101289	+	729.00	1478.58	4.1e-73	690	! BI101289 602887019F1 NCI_CGAP_K
gb_gss:CNS03W7V	-	690.50	1398.14	1.2e-68	753	! AL263380 Tetraodon nigroviridis
gb_est1:AV603377	+	674.50	1368.45	5.6e-67	575	! AV603377 AV603377 Bos taurus ki
gb_est1:AV602053	+	671.50	1359.18	1.8e-66	740	! AV602053 AV602053 Bos taurus ki
gb_est1:AW226791	+	656.00	1331.23	6.6e-65	533	! AW226791 um62c03.y1 Sugano mous
gb_est1:AW318913	+	644.00	1305.07	1.9e-63	599	! AW318913 un09d03.y1 Sugano mous
gb_est1:AW107090	+	641.50	1300.29	3.5e-63	581	! AW107090 ul92g12.y1 Sugano mous
gb_est1:AI747352	+	638.00	1297.69	4.9e-63	398	! AI747352 ul05d05.y1 Sugano mous
gb_est1:AI227094	+	625.00	1267.51	2.4e-61	525	! AI227094 uj11g11.y1 Sugano mous
gb_est2:BI550775	+	622.50	1257.61	8.4e-61	774	! BI550775 603195669F1 NIH_MGC_95
gb_est1:AL667662	+	612.50	1234.68	1.6e-59	935	! AL667662 AL667662 directional l
gb_est1:BB622505	+	608.00	1230.02	2.9e-59	641	! BB622505 BB622505 RIKEN full-le
gb_gss:CNS03UQB	-	608.00	1224.22	6.1e-59	1030	! AL261452 Tetraodon nigroviridi
gb_est2:BF780894	+	604.00	1217.64	1.4e-58	899	! BF780894 602105404F1 NCI_CGAP_K
gb_htc:AK015481	+	596.00	1197.50	1.9e-57	1212	! AK015481 Mus musculus adult ma
gb_htc:AK015907	+	595.00	1192.37	3.6e-57	1557	! AK015907 Mus musculus adult ma
gb_gss:AQ222870	+	589.00	1194.87	2.6e-57	461	! AQ222870 HS_2014_A2_H08_MR CIT
gb_est1:AA989815	+	580.00	1175.72	3.1e-56	484	! AA989815 uc79d07.y1 Sugano mous
gb_est1:AW259349	+	549.00	1111.59	1.1e-52	493	! AW259349 um92d02.y1 Sugano mous
gb_est1:AW259025	+	544.00	1102.61	3.6e-52	442	! AW259025 um76e01.y1 Sugano mous
gb_est2:BG394461	+	528.50	1069.17	5.7e-50	816	! BG394461 602456988F1 NIH_MGC_16
gb_est1:AI788269	+	521.50	1051.61	2.5e-49	645	! AI788269 uk56a04.y1 Sugano mous
gb_est1:AL583547	+	517.50	1037.77	1.5e-48	1019	! AL583547 AL583547 LTI_FL015_Br
gb_est1:AW012077	+	511.50	1033.48	2.6e-48	526	! AW012077 um07e03.y1 Sugano mous
gb_est1:AL528489	+	502.50	1006.79	7.8e-47	1024	! AL528489 AL528489 LTI_NFL003_N
gb_est2:BI546348	+	502.00	1006.04	8.6e-47	1001	! BI546348 603188840F1 NIH_MGC_9
gb_est2:BG972732	+	492.50	988.04	8.7e-46	879	! BG972732 602837519F1 NCI_CGA
gb_est2:BG253799	+	491.50	984.95	1.3e-45	956	! BG253799 602366683F1 NIH_MGC_
gb_gss:CNS02DYX	+	490.50	982.65	1.7e-45	975	! AL193074 Tetraodon nigroviri
gb_gss:AQ471589	-	490.00	987.67	9.1e-46	594	! AQ471589 CITBI-E1-2588J18.TR
gb_est1:BE237514	+	489.50	988.24	8.5e-46	521	! BE237514 146834 MARC 4BOV Bo

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seq_name: gb_est2:BI143740

seq_documentation_block:
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DEFINITION  602907395F1 NCI_CGAP_Kid14 Mus musculus cDNA clone IMAGE:5064407
            5', mRNA sequence.
ACCESSION   BI143740
VERSION     BI143740.1  GI:14603741
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 858)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Jeffrey E. Green, M.D.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM11173  row: n  column: 24
            High quality sequence stop: 854.
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                     /clone="IMAGE:5064407"
                     /clone_lib="NCI_CGAP_Kid14"
                     /lab_host="DH10B (T1 phage-resistant)"
                     /note="Organ: kidney; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally.  Primer: Oligo dT.
                     Average insert size 1.75 kb. Constructed by Life
                     Technologies. Note: this is a NCI_CGAP Library. |"
BASE COUNT      227 a    220 c    201 g    210 t
ORIGIN


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              Ratio:  4.659                 Gaps:      6
 Percent Similarity:  95.455   Percent Identity: 90.210

alignment_block:
 US-09-623-304A-1 x BI143740   ..

 Align seg 1/1  to: BI143740  from: 1  to: 858

      87 IlePheGlySerValPheTrpLeuIleAlaPheHisHisGlyAspLeuLe 103
         ||||||||||||:::|||||||||||||||||||||||||||||||||||
       3 ATATTTGGTTCCATATTTTGGCTCATAGCCTTTCATCACGGAGACCTATT 52

     103 u.AsnAspProAspIleThrProCysValAspAsnValHisSerPheThr 119
         | :::|||||||||||||||||||||||||||||||||||||||||||||
      53 AACGCGATCCAGATATCACCCCTTGTGTTGACAACGTGCATTCATTTACG 102

     120 GlyAlaPheLeuPheSerLeuGluThrGlnThrThrIleGlyTyrGlyTy 136
         :::|||||||||||||||||||||||||||||||||||||||||||||||
     103 GCTGCATTTTTATTCTCCCTGGAGACCCAGACCACCATTGGATACGGTTA 152

     136 rArgCysValThrGluGluCysSerValAlaValLeuMetValIleLeuG 153
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     ||||||||||||||||||||||||||||||||||||||    ||||||||||
 153 CCGCTGTGTCACCGAAGAGTGCTCTGTGGCTGTACTGACAGTGATCCTTC 202

 153 lnSerIleLeuSerCysIleIleAsnThrPheIleIleGlyAlaAlaLeu 169
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 203 AGTCCATCCTCAGCTGCATCATAAACACCTTCATCATTGGAGCAGCCTTG 252

 170 AlaLysMetAlaThrAlaArgLysArgAlaGlnThrIleArgPheSerTy 186
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 253 GCAAAGATGGCAACTGCCCGGAAGAGAGCCCAGACCATACGCTTCAGCTA 302

 186 rPheAlaLeuIleGlyMetArgAspGlyLysLeuCysLeuMetTrpArgI 203
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 303 TTTTGCCCTCATTGGTATGAGAGACGGGAAGCTTTGCCTCATGTGGCGCA 352

 203 leGlyAspPheArgProAsnHisValValGluGlyThrValArgAlaGln 219
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 353 TAGGTGACTTCCGACCAAACCATGTGGTAGAGGGCACGGTGAGAGCCCAA 402

 220 LeuLeuArgTyrThrGluAspSerGluGlyArgMetThrMetAlaPheLy 236
     |||||||||||:::||||||||||||||||||||||||||||||||||||
 403 CTTCTGCGCTATTCAGAAGACAGTGAAGGGAGGATGACGATGGCGTTTAA 452

 236 sAspLeuLysLeuValAsnAspGlnIleIleLeuValThrProValThrI 253
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 453 AGACCTCAAACTCGTCAATGACCAGATAATCCTGGTAACTCCAGTGACTA 502

 253 leValHisGluIleAspHisGluSerProLeuTyrAlaLeuAspArgLys 269
     |||||||:::||||||||||||||||||||||||||||||||||||||||
 503 TTGTCCATGACATTGACCATGAGAGCCCTCTGTATGCCCTTGACCGCAAG 552

 270 AlaValAlaLysAspAsnPheGluIleLeuValThrPheIleTyrThrGl 286
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 553 GCAGTGGCCAAAGATAATTTCGAGATTCTGGTGACATTTATTTATACTGG 602

 286 yAspSerThrGlyThrSerHisGlnSerArgSerSerTyrValProArg* 303
     ||||||||||||||||||||||||||||||||||||||||:::||||||
 603 TGATTCCACTGGGACATCCCACCAGTCCAGAAGTTCCTACATCCCCAGAG 652

 303 **IleLeuTrpGlyHisArgPheAsnAspValLeuGluValLysArgLys 319
       ||||||||||||||||||||:::||||||    ||||||   :::|||
 653 AAATTCTCTGGGGCCACAGGTTTCATGATGTATCGGAAGTGACAGAGAAA 702

 320 ..TyrTyrLysValAsnCysLeuGln.PheGluGlySerValGluValTy 335
       ||||||||||||||||||||||||| ||||||||||||||||||||||
 703 CGTACTACAAGGTGAACTGCTTGCAAGTTTGAAGGAAGCGTGGAAGTCTA 752

 335 rAla.ProPheCysSerAla.LysGlnLeuAspTrpLysAspGlnGlnLe 351
     |||| ||||||||||||||| ||||||||||||||||||||||||||::
 753 CGCCCCCCTTTTGCAGTGCCAAAACAACTGGACTGGAAGGACCAACAATT 802

 351 uHis..IleGluLysAlaProProValArgGluSerCysThrSerAsp 366
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seq_name: gb_est2:BI144257

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seq_documentation_block:
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DEFINITION  602907822F1 NCI_CGAP_Kid14 Mus musculus cDNA clone IMAGE:5064724
            5', mRNA sequence.
ACCESSION   BI144257
VERSION     BI144257.1  GI:14604258
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 781)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Jeffrey E. Green, M.D.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM11174  row: 1  column: 05
            High quality sequence start: 25
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                     /clone_lib="NCI_CGAP_Kid14"
                     /lab_host="DH10B (T1 phage-resistant)"
                     /note="Organ: kidney; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally.  Primer: Oligo dT.
                     Average insert size 1.75 kb. Constructed by Life
                     Technologies. Note: this is a NCI_CGAP Library. |"
BASE COUNT      204 a    184 c    188 g    205 t
ORIGIN


alignment_scores:
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             Ratio:   4.991                Gaps:      2
 Percent Similarity:  96.970   Percent Identity: 91.775

alignment_block:
 US-09-623-304A-1 x BI144257   ..

 Align seg 1/1  to: BI144257  from: 1  to: 781

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      89 ATGAGCTATTACGGAAGTAGCTACAGGATTGTCAATGTGGACTCCAAATA 138

      17 rProGlyTyrProProGluHisIleIleAlaGluLysArgArgAlaArgA 34
         |||||||||||||||||||||    |||||||||||||||||||||||||
     139 TCCAGGCTATCCTCCAGAGCATGCCATCGCTGAGAAGAGAAGAGCAAGAA 188

      34 rgArgLeuLeuHisLysAspGlySerCysAsnValTyrPheLysHisIle 50
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     189 GGCGCTTGCTCCACAAAGATGGCAGCTGTAATGTGTACTTTAAACACATT 238

      51 PheGlyGluTrpGlySerTyrValValAspIlePheThrThrLeuValAs 67
         ||||||||||||||||||||:::|||||||||||||||||||||||||||
     239 TTTGGAGAATGGGGGAGCTACATGGTTGATATTTTTACCACTCTTGTGGA 288

      67 pThrLysTrpArgHisMetPheValIlePheSerLeuSerTyrIleLeuS 84
         ||||||||||||||||||||:::|||||||||||||||||||||||||||
     289 TACCAAGTGGCGCCATATGTTCATAATATTTTCTCTGTCTTACATTCTCT 338

      84 erTrpLeuIlePheGlySerValPheTrpLeuIleAlaPheHisHisGly 100
         ||||||||||||||||||||:::|||||||||||||||||||||||||||
     339 CCTGGTTGATATTTGGTTCCATATTTGGCTCATAGCCTTTCATCACGGA 388

     101 AspLeuLeuAsnAspProAspIleThrProCysValAspAsnValHisSe 117
         ||||||||:::|||||||||||||||||||||||||||||||||||||||
     389 GACCTATTAAGCGATCCAGATATCACCCCTTGTGTTGACAACGTGCATTC 438

     117 rPheThrGlyAlaPheLeuPheSerLeuGluThrGlnThrThrIleGlyT 134
         ||||||:::|||||||||||||||||||||||||||||||||||||||||
     439 ATTTACGGCTGCATTTTTATTCTCCCTGGAGACCCAGACCACCATTGGAT 488

     134 yrGlyTyrArgCysValThrGluGluCysSerValAlaValLeuMetVal 150
         ||||||||||||||||||||||||||||||||||||||||||    |||
     489 ACGGTTACCGCTGTGTCACCGAAGAGTGCTCTGTGGCTGTACTGACAGTG 538
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     151 IleLeuGlnSerIleLeuSerCysIleIleAsnThrPheIleIleGlyAl 167
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     539 ATCCTTCAGTCCATCCTCAGCTGCATCATAAACACCTTCATCATTGGAGC 588

     167 aAlaLeuAlaLysMetAlaThrAlaArgLysArgAlaGlnThrIleArgP 184
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     589 AGCCTTGGCAAAGATGGCAACTGCCCGGAAGAGAGCCCAGACCATACGCT 638

     184 heSerTyrPheAlaLeuIleGlyMetArgAspGlyLysLeuCys.LeuMe 200
         ||||||||||||||||||||||||||||||||||||||    |||||
     639 TCAGCTATTTTGCCCTCATTGGTATGAGAGACGGGAAGCTTTGGCCTCAT 688

     200 tTrpArgIleGlyAspPheArgProAsnHisValValGluGlyThrValA 217
         ||||||||||||||||||||   ||||||||||||||||||||||||||
     689 GTGGCGCATAGGTGACTTCCGAACAAACCATGTGGTAGAGGGCACGGTGA 738

     217 rgAlaGlnLeuLeuArgTyrThrGluAspSerGluGlyArg 230
         ||||||||||||||||||      ::::::::::||||||
     739 GAGCCCAACTTCTGCGCTAT......CAGAAGAAAGGAAGG 773

seq_name: gb_est2:BI143982

seq_documentation_block:
LOCUS       BI143982               753 bp    mRNA    linear   EST 05-JUL-2001
DEFINITION  602908077F1 NCI_CGAP_Kid14 Mus musculus cDNA clone IMAGE:5065051
            5', mRNA sequence.
ACCESSION   BI143982
VERSION     BI143982.1  GI:14603983
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 753)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Jeffrey E. Green, M.D.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM11175  row: i  column: 20
            High quality sequence stop: 725.
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                     /lab_host="DH10B (T1 phage-resistant)"
                     /note="Organ: kidney; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally.  Primer: Oligo dT.
                     Average insert size 1.75 kb. Constructed by Life
                     Technologies. Note: this is a NCI_CGAP Library. |"
BASE COUNT      212 a    166 c    171 g    204 t
ORIGIN


alignment_scores:
           Quality:  979.00             Length:    210
             Ratio:  4.847                Gaps:      2
 Percent Similarity:  96.190   Percent Identity: 89.524

alignment_block:
 US-09-623-304A-1 x BI143982   ..

 Align seg 1/1  to: BI143982  from: 1  to: 753
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     127 ATGAGCTATTACGGAAGTAGCTACAGGATTGTCAATGTGGACTCCAAATA 176

      17 rProGlyTyrProProGluHisIleIleAlaGluLysArgArgAlaArgA 34
         ||||||||||||||||||||   ||||||||||||||||||||||||||
     177 TCCAGGCTATCCTCCAGAGCATGCCATCGCTGAGAAGAGAAGAGCAAGAA 226

      34 rgArgLeuLeuHisLysAspGlySerCysAsnValTyrPheLysHisIle 50
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     227 GGCGCTTGCTCCACAAAGATGGCAGCTGTAATGTGTACTTTAAACACATT 276

      51 PheGlyGluTrpGlySerTyrValValAspIlePheThrThrLeuValAs 67
         ||||||||||||||||||||:::||||||||||||||||||||||||||
     277 TTTGGAGAATGGGGGAGCTACATGGTTGATATTTTTACCACTCTTGTGGA 326

      67 pThrLysTrpArgHisMetPheValIlePheSerLeuSerTyrIleLeuS 84
         ||||||||||||||||||||::||||||||||||||||||||||||||||
     327 TACCAAGTGGCGCCATATGTTCATAATATTTTCTCTGTCTTACATTCTCT 376

      84 erTrpLeuIlePheGlySerValPheTrpLeuIleAlaPheHisHisGly 100
         ||||||||||||||||||:::||||||||||||||||||||||||||||
     377 CCTGGTTGATATTTGGTTCCATATTTTGGCTCATAGCCTTTCATCACGGA 426

     101 AspLeuLeuAsnAspProAspIleThrProCysValAspAsnValHisSe 117
         |||||||||:::||||||||||||||||||||||||||||||||||||||
     427 GACCTATTAAGCGATCCAGATATCACCCCTTGTGTTGACAACGTGCATTC 476

     117 rPheThrGlyAlaPheLeuPheSerLeuGluThrGlnThrThrIleGlyT 134
         |||||||:::||||||||||||||||||||||||||||||||||||||||
     477 ATTTACGGCTGCATTTTTATTCTCCCTGGAGACCCAGACCACCATTGGAT 526

     134 yrGlyTyrArgCysValThrGluGluCysSerValAlaValLeuMetVal 150
         ||||||||||||||||||||||||||||||||||||||||||||   |||
     527 ACGGTTACCGCTGTGTCACCGAAGAGTGCTCTGTGGCTGTACTGACAGTG 576

     151 IleLeuGlnSerIleLeuSerCysIleIleAsnThrPheIleIleGlyAl 167
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     577 ATCCTTCAGTCCATCCTCAGCTGCATCATAAACACCTTCATCATTGGAGC 626

     167 aAlaLeuAlaLysMetAlaThr.AlaArgLysArgAlaGlnThrIle.Ar 183
         |||||||||||||||||||| |||||||||::::::|||||||||
     627 AGCCTTGGCAAAGATGGCAACTTGCCCGGAAAGAGAGCCAGACCATAAGC 676

     183 gPheSerTyrPheAlaLeuIleGlyMetArgAspGlyLysLeuCysLeuM 200
         |||   |||:::||||||   ||||||||||||||||||   |||||||
     677 GTTCAGGTATTTGGCCCTCTATGGTATGAGAGACGGGAAGTT.TGCCTCA 725

     200 etTrpArgIleGlyAspPheArgPro 208
         |||||   ||||||:::|||||||||
     726 TGTGGGGAATAGGTGAATTCCGACCA 751

seq_name: gb_est2:BI101237

seq_documentation_block:
LOCUS       BI101237               662 bp    mRNA    linear   EST 26-JUN-2001
DEFINITION  602886939F1 NCI_CGAP_Kid14 Mus musculus cDNA clone IMAGE:5042480
            5', mRNA sequence.
ACCESSION   BI101237
VERSION     BI101237.1  GI:14552130
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 662)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Jeffrey E. Green, M.D.
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            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
           found through the I.M.A.G.E. Consortium/LLNL at:
           http://image.llnl.gov
           Plate: LLAM11116  row: m  column: 09
           High quality sequence start: 24
           High quality sequence stop: 660.
FEATURES             Location/Qualifiers
     source          1. .662
                     /organism="Mus musculus"
                     /strain="FVB/N"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:5042480"
                     /clone_lib="NCI_CGAP_Kid14"
                     /lab_host="DH10B (T1 phage-resistant)"
                     /note="Organ: kidney; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally.  Primer: Oligo dT.
                     Average insert size 1.75 kb. Constructed by Life
                     Technologies. Note: this is a NCI_CGAP Library. |"
BASE COUNT      160 a    168 c    152 g    182 t
ORIGIN


alignment_scores:
            Quality:  972.50            Length:    216
              Ratio:  4.698               Gaps:      5
 Percent Similarity:  95.833   Percent Identity: 89.815

alignment_block:
 US-09-623-304A-1 x BI101237   ..

 Align seg 1/1  to: BI101237  from: 1  to: 662

      52 GlyGluTrpGlySerTyrValValAspIlePheThrThrLeuValAspTh 68
         ||||||||||||||||||:::||||||||||||||||||||||||||||||
      23 GGAGAATGGGGGAGCTACATGGTTGATATTTTTACCACTCTTGTGGATAC 72

      68 rLysTrpArgHisMetPheValIlePheSerLeuSerTyrIleLeuSerT 85
         ||||||||||||||||||:::||||||||||||||||||||||||||||||
      73 CAAGTGGCGCCATATGTTCATAATATTTTCTCTGTCTTACATTCTCTCCT 122

      85 rpLeuIlePheGlySerValPheTrpLeuIleAlaPheHisHisGlyAsp 101
         ||||||||||||||||||:::||||||||||||||||||||||||||||||
     123 GGTTGATATTTGGTTCCATATTTTGGCTCATAGCCTTTCATCACGGAGAC 172

     102 LeuLeuAsnAspProAspIleThrProCysValAspAsnValHisSerPh 118
         ||||||:::||||||||||||||||||||||||||||||||||||||||||
     173 CTATTAAGCGATCCAGATATCACCCCTTGTGTTGACAACGTGCATTCATT 222

     118 eThrGlyAlaPheLeuPheSerLeuGluThrGlnThrThrIleGlyTyrG 135
         ||||:::||||||||||||||||||||||||||||||||||||||||||||
     223 TACGGCTGCATTTTTATTCTCCCTGGAGACCCAGACCACCATTGGATACG 272

     135 lyTyrArgCysValThrGluGluCysSerValAlaValLeuMetValIle 151
         ||||||||||||||||||||||||||||||||||||||||   ||||||
     273 GTTACCGCTGTGTCACCGAAGAGTGCTCTGTGGCTGTACTGACAGTGATC 322

     152 LeuGlnSerIleLeuSerCysIleIleAsnThrPheIleIleGlyAlaAl 168
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     323 CTTCAGTCCATCCTCAGCTGCATCATAAACACCTTCATCATTGGAGCAGC 372

     168 aLeuAla.LysMetAlaThrAlaArgLysArgAlaGlnThrIleArgPhe 184
         |||||||.||||||||||||||||||||||||||||||||||||||||||
     373 CTTGGCCAAAGATGGCAACTGCCCGGAAGAGAGCCCAGACCATACGCTTC 422

     185 SerTyrPheAlaLeuIleGlyMetArg.AspGlyLys.LeuCysLeuMet 200
         |||||||||||||||||||||||||.|||||::: |||||||||||||
     423 AGCTATTTTGCCCTCATTGGTATGAGACGACGGGAACGCTTTGCCTCATG 472

     201 TrpArgIleGlyAspPheArgProAsnHisValValGluGly...ThrVa 216
         ||||||||||||||||||||||||||||||||||:::|||      ::

     473 TGGCGCATAGGTGACTTCCGACCAAACCATGTGGTCAGAGGGCACGGTGC 522

     216 lArgAlaGlnLeuLeuArgTyrThrGluAspSerGluGlyArgMetThrM 233
         ::::      ||||||||||||:::||||||||:::|||||||||||||
     523 AGAGCCCACACTTCTGCGCTATTCAGAAGACAGTGACGGGAGGATGACGA 572

     233 etAlaPhe.LysAspLeuLysLeuValAsnAspGlnIleIleLeuValTh 249
         |||||||| :::||||||||||||||||||||||||||||||||||||||
     573 TGGCGTTTACAAGACCTCAAACTCGTCAATGACCAGATAATCCTGGTAAC 622

     249 rProValThrIleValHisGluIleAspHisGluSerPro 262
         ||||||||||||||||||:::|||||||||||||||||||
     623 TCCAGTGACTATTGTCCATGACATTGACCATGAGAGCCCT 662

seq_name: gb_est2:BI101492

seq_documentation_block:
LOCUS       BI101492                686 bp    mRNA    linear   EST 26-JUN-2001
DEFINITION  602887284F1 NCI_CGAP_Kid14 Mus musculus cDNA clone IMAGE:5042372
            5', mRNA sequence.
ACCESSION   BI101492
VERSION     BI101492.1  GI:14552385
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 686)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Jeffrey E. Green, M.D.
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
           found through the I.M.A.G.E. Consortium/LLNL at:
           http://image.llnl.gov
           Plate: LLAM11116  row: h  column: 21
           High quality sequence stop: 684.
FEATURES             Location/Qualifiers
     source          1. .686
                     /organism="Mus musculus"
                     /strain="FVB/N"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:5042372"
                     /clone_lib="NCI_CGAP_Kid14"
                     /lab_host="DH10B (T1 phage-resistant)"
                     /note="Organ: kidney; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally.  Primer: Oligo dT.
                     Average insert size 1.75 kb. Constructed by Life
                     Technologies. Note: this is a NCI_CGAP Library. |"
BASE COUNT      194 a    155 c    150 g    187 t
ORIGIN


alignment_scores:
            Quality:  934.00            Length:    188
              Ratio:  5.049               Gaps:      0
 Percent Similarity:  98.404   Percent Identity: 92.021

alignment_block:
 US-09-623-304A-1 x BI101492   ..

 Align seg 1/1  to: BI101492  from: 1  to: 686

       1 MetSerTyrTyrGlySerSerTyrHisIleIleAsnAlaAspAlaLysTy 17
         ||||||||||||||||||||||:::|||:::|||:::|||:::||||||
     109 ATGAGCTATTACGGAAGTAGCTACAGGATTGTCAATGTGGACTCCAAATA 158

      17 rProGlyTyrProProGluHisIleIleAlaGluLysArgArgAlaArgA 34
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     159 TCCAGGCTATCCTCCAGAGCATGCCATCGCTGAGAAGAGAAGAGCAAGAA 208

      34 rgArgLeuLeuHisLysAspGlySerCysAsnValTyrPheLysHisIle 50
     209 GGCGCTTGATCCACAAAGATGGCAGCTGTAATGTGTACTTTAAACACATT 258

      51 PheGlyGluTrpGlySerTyrValValAspIlePheThrThrLeuValAs 67
     259 TTTGGAGAATGGGGGAGCTACATGGTTGATATTTTTACCACTCTTGTGGA 308

      67 pThrLysTrpArgHisMetPheValIlePheSerLeuSerTyrIleLeuS 84
     309 TACCAAGTGGCGCCATATGTTCATAATATTTTCTCTGTCTTACATTCTCT 358

      84 erTrpLeuIlePheGlySerValPheTrpLeuIleAlaPheHisHisGly 100
     359 CCTGGTTGATATTTGGTTCCATATTTAGGCTCATAGCCTTTCATCACGGA 408

     101 AspLeuLeuAsnAspProAspIleThrProCysValAspAsnValHisSe 117
     409 GACCTATTAAGCGATCCAGATATCACCCCTTGTGTTGACAACGTGCATTC 458

     117 rPheThrGlyAlaPheLeuPheSerLeuGluThrGlnThrThrIleGlyT 134
     459 ATTTACGGCTGCATTTTTATTCTCCCTGGAGACCCAGACCACCATTGGAT 508

     134 yrGlyTyrArgCysValThrGluGluCysSerValAlaValLeuMetVal 150
     509 ACGGTTACCGCTGTGTCACCGAAGAGTGCTCTGTGGCTGTACTGACAGTG 558

     151 IleLeuGlnSerIleLeuSerCysIleIleAsnThrPheIleIleGlyAl 167
     559 ATCCTTCAGTCCATCCTCAGCTGCATCATAAACACCTTCATCATTGGAGC 608

     167 aAlaLeuAlaLysMetAlaThrAlaArgLysArgAlaGlnThrIleArgP 184
     609 AGGCTTGGCAAAGATGGCAACTGCCCGGAAGAGAGCCCAGACCATACGCT 658

     184 heSerTyrPheAla 188
     659 TCAGCTATATTGCC 672

seq_name: gb_est2:BF780854

seq_documentation_block:
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DEFINITION  602105743F1 NCI_CGAP_Kid14 Mus musculus cDNA clone IMAGE:4223626
            5', mRNA sequence.
ACCESSION   BF780854
VERSION     BF780854.1  GI:12085887
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 710)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Jeffrey E. Green, M.D.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM9812  row: f  column: 11
            High quality sequence stop: 703.
FEATURES             Location/Qualifiers
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                     /clone="IMAGE:4223626"
                     /clone_lib="NCI_CGAP_Kid14"
                     /lab_host="DH10B (T1 phage-resistant)"
                     /note="Organ: kidney; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally.  Primer: Oligo dT.
                     Average insert size 1.75 kb. Constructed by Life
                     Technologies. Note: this is a NCI_CGAP Library. |"
BASE COUNT      198 a    177 c    177 g    158 t
ORIGIN


alignment_scores:
            Quality:  916.50             Length:    190
              Ratio:  4.927                Gaps:      1
 Percent Similarity:  97.895   Percent Identity: 92.105

alignment_block:
 US-09-623-304A-1 x BF780854   ..

 Align seg 1/1  to: BF780854  from: 1  to: 710

     194 AspGlyLysLeuCysLeuMetTrpArgIleGlyAspPheArgProAsnHi 210
       2 GACGGGAAGCTTTGCCTCATGTGGCGCATAGGTGACTTCCGACCAAACCA 51

     210 sValValGluGlyThrValArgAlaGlnLeuLeuArgTyrThrGluAspS 227
      52 TGTGGTAGAGGGCACGGTGAGAGCCCAACTTCTGCGCTATTCAGAAGACA 101

     227 erGluGlyArgMetThrMetAlaPheLysAspLeuLysLeuValAsnAsp 243
     102 GTGAAGGGAGGATGACGATGGCGTTTAAAGACCTCAAACTCGTCAATGAC 151

     244 GlnIleIleLeuValThrProValThrIleValHisGluIleAspHisGl 260
     152 CAGATAATCCTGGTAACTCCAGTGACTATTGTCCATGAAATTGACCATGA 201

     260 uSerProLeuTyrAlaLeuAspArgLysAlaValAlaLysAspAsnPheG 277
     202 GAGCCCTCTGTATGCCCTTGACCGCAAGGCAGTGGCCAAAGATAATTTCG 251

     277 luIleLeuValThrPheIleTyrThrGlyAspSerThrGlyThrSerHis 293
     252 AGATTCTGGTGACATTTATTTATACTGGTGATTCCACTGGGACATCCCAC 301

     294 GlnSerArgSerSerTyrValProArg***IleLeuTrpGlyHisArgPh 310
     302 CAGTCCAGAAGTTCCTACATCCCCAGAGAAATTCTCTGGGGCCACAGGTT 351

     310 eAsnAspValLeuGluValLysArgLysTyrTyrLysValAsnCysLeuG 327
     352 TCATGATGTATTGGAAGTGAAGAGAAAGTACTACAAGGTGAACTGCTTGC 401

     327 lnPheGluGlySerValGluValTyrAlaProPheCysSerAlaLysGln 343
     402 AGTTTGAAGGAAGCGTGGAAGTCTACGCCCCCTTTTGCAGTGCCAAACAA 451

     344 LeuAspTrpLysAspGlnGlnLeu...HisIleGluLysAlaProProVa 359
     452 CTGGACTGGAAGGACCAACAACTCAACAACTTGGAGAAAACGTCCCCTGC 501

     359 lArgGluSerCysThrSerAspThrLysAlaArgArgArgSerPheSerA 376
     502 CCGAGGATCCTGCAATTCTGACACCAACACCAGGAGGCGGTCCTTCAGCG 551

     376 laValAlaIleValSerSer 382
     552 CAGTTGCTGTGGTGAGCAGC 571

seq_name: gb_est2:BF789666
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seq_documentation_block:
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DEFINITION  602105281F1 NCI_CGAP_Kid14 Mus musculus cDNA clone IMAGE:4223157
            5', mRNA sequence.
ACCESSION   BF789666
VERSION     BF789666.1  GI:12094702
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 783)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Jeffrey E. Green, M.D.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM9811  row: b  column: 22
            High quality sequence stop: 721.
FEATURES             Location/Qualifiers
     source          1. .783
                     /organism="Mus musculus"
                     /strain="FVB/N"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:4223157"
                     /clone_lib="NCI_CGAP_Kid14"
                     /lab_host="DH10B (T1 phage-resistant)"
                     /note="Organ: kidney; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally.  Primer: Oligo dT.
                     Average insert size 1.75 kb. Constructed by Life
                     Technologies. Note: this is a NCI_CGAP Library. |"
BASE COUNT      216 a    176 c    181 g    210 t
ORIGIN


alignment_scores:
            Quality:  896.50             Length:    208
              Ratio:  4.574                Gaps:      7
 Percent Similarity:  94.231   Percent Identity: 87.019

alignment_block:
 US-09-623-304A-1 x BF789666   ..

 Align seg 1/1  to: BF789666  from: 1  to: 783

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         ||||||||||||||||||||||||:::|||:::|||:::|||:::|||||
     147 ATGAGCTATTACGGAAGTAGCTACAGGATTGTCAATGTGGACTCCAAATA 196

      17 rProGlyTyrProProGluHisIleIleAlaGluLysArgArgAlaArgA 34
         ||||||||||||||||||||   ||||||||||||||||||||||||||
     197 TCCAGGCTATCCTCCAGAGCATGCCATCGCTGAGAAGAGAAGAGCAAGAA 246

      34 rgArgLeuLeuHisLysAspGlySerCysAsnValTyrPheLysHisIle 50
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     247 GGCGCTTGCTCCACAAAGATGGCAGCTGTAATGTGTACTTTAAACACATT 296

      51 PheGlyGluTrpGlySerTyrValValAspIlePheThrThrLeuValAs 67
         ||||||||||||||||||||:::|||||||||||||||||||||||||||
     297 TTTGGAGAATGGGGGAGCTACATGGTTGATATTTTTACCACTCTTGTGGA 346

      67 pThrLysTrpArgHisMetPheValIlePheSerLeuSerTyrIleLeuS 84
         ||||||||||||||||||||||:::|||||||||||||||||||||||||
     347 TACCAAGTGGCGCCATATGTTCATAATATTTTCTCTGTCTTACATTCTCT 396

      84 erTrpLeuIlePheGlySerValPheTrpLeuIleAlaPheHisHisGly 100
         ||||||||||||||||||||||:::|||||||||||||||||||||||||||
     397 CCTGGTTGATATTTGGTTCCATATTTTGGCTCATAGCCTTTCATCACGGA 446

     101 AspLeuLeuAsnAspProAspIleThrProCysValAspAsnValHisSe 117
         |||||||||:::|||||||||||||||||||||||||||||||||||||||
     447 GACCTATTAAGCGATCCAGATATCACCCCTTGTGTTGACAACGTGCATTC 496

     117 rPheThrGlyAlaPheLeuPheSerLeuGluThrGlnThrThrIleGlyT 134
         |||||||:::|||||||||||||||||||||||||||||||||||||||||
     497 ATTTACGGCTGCATTTTTATTCTCCCTGGAGACCCAGACCACCATTGGAT 546

     134 yrGlyTyrArgCysValThr.GluGluCysSerValAlaValLeuMetVa 150
         |||||||||||||||||| ||||||||||||||||||||||   ||
     547 ACGGTTACCGCTGTGTCACCCGAAGAGTGCTCTGTGGCTGTACTGACAGT 596

     150 lIleLeuGlnSerIle.LeuSerCysIleIle.AsnThrPheIleIleGl 166
         |||||||||||||||| ||||||||||||| |||||||||||||||||
     597 GATCCTTCAGTCCATCCCTCAGCTGCATCATAAAACACCTTCATCATTGG 646

     166 yAlaAla.LeuAlaLysMetAlaThrAlaArgLys.ArgAlaGlnThr.I 182
         ||||||| |||||||||||:::|||||||||| |||:::|||||| |
     647 AGCAGCCTTTGGCAAAGATGGGCACTGCCCGGAAGGAGAAGCCAGACCAA 696

     182 leArgPheSerTyrPheAlaLeuIleGlyMet...ArgAspGlyLysLeu 197
         ||   |||||||||:::|||||||||   :::   |||   |||::::::
     697 TAAGCTTCAGTTATTTGGCCCTCATTTGGTTTGAAAGACGGGGAAACTTT 746

     198 CysLeuMetTrp 201
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     747 TGCCTCATGTGG 758

seq_name: gb_est2:BF411612

seq_documentation_block:
LOCUS       BF411612                516 bp    mRNA    linear   EST 28-NOV-2000
DEFINITION  UI-R-BT1-bmp-d-10-0-UI.s1 UI-R-BT1 Rattus norvegicus cDNA clone
            UI-R-BT1-bmp-d-10-0-UI 3', mRNA sequence.
ACCESSION   BF411612
VERSION     BF411612.1  GI:11399601
KEYWORDS    EST.
SOURCE      Norway rat.
  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
REFERENCE   1  (bases 1 to 516)
  AUTHORS   Bonaldo,M.F., Lennon,G. and Soares,M.B.
  TITLE     Normalization and subtraction: two approaches to facilitate gene
            discovery
  JOURNAL   Genome Res. 6 (9), 791-806 (1996)
  MEDLINE   97044477
COMMENT     Contact: Soares, MB
            Program for Rat Gene Discovery and Mapping
            University of Iowa
            451 Eckstein Medical Research Building Iowa City, IA 52242, USA
            Tel: 319 335 8250
            Fax: 319 335 9565
            Email: msoares@blue.weeg.uiowa.edu
            The sequence contained an oligo-dT track that was present in the
            oligonucleotide that was used to prime the synthesis of first
            strand cDNA and therefore this may represent a bonafide poly A
            tail. The sequence tag present in the cDNA between the NotI site
            and the oligo-dT track served to identify it as a clone from the
            normalized mid-brain library cDNA Library Preparation: M.B. Soares
            Lab Clone distribution: clones will be available through Research
            Genetics (www.resgen.com)
            Seq primer: M13 Forward
            POLYA=Yes.
FEATURES             Location/Qualifiers
     source          1. .516
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                     /strain="Sprague-Dawley"
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                     /dev_stage="adult"
                     /lab_host="DH10B (Life Technologies)"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; Site_1: Not I; Site_2: Eco RI; The library
                     UI-R-BT1 is a subtracted library derived from a mixture of
                     the following tissues: hippocampus, thalamus, mid-brain,
                     medulla, corpus striatum, cerebral cortex and testis. For
                     a detailed description of the library from  which this
                     clone was derived, please visit our web site at
                     ratest.eng.uiowa.edu. The subtraction has been previously
                     described in (Bonaldo, Lennon and Soares, Genome Research
                     6:791-806, 1996)
                     TAG_LIB=UI-R-BT1
                     TAG_TISSUE=mid-brain
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BASE COUNT      126 a    124 c    138 g    128 t
ORIGIN


alignment_scores:
            Quality:  830.00             Length:    168
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alignment_block:
 US-09-623-304A-1 x BF411612/rev   ..

 Align seg 1/1  to reverse of: BF411612  from: 1  to: 516

      72 HisMetPheValIlePheSerLeuSerTyrIleLeuSerTrpLeuIlePh 88
         |||||||||||||||||||||||||||   ||||||||||||||||||||
     516 CATATGTTTGTAATATTTTCTTTGTCTAACATTCTCTCCTGGTTGATATT 467

      88 eGlySerValPheTrpLeuIleAlaPheHisHisGlyAspLeuLeuAsnA 105
         ||||   :::|||||||||||||||:::|||||||||||||||||||:::|
     466 CGGCCCCATATTTTGGCTCATAGCCCTTCATCACGGAGACCTATTAAGCG 417

     105 spProAspIleThrProCysValAspAsnValHisSerPheThrGlyAla 121
         |||||||||||||||||||||||||||||||||||||||||||||:::|||
     416 ATCCAGACATCACCCCGTGCGTGGACAACGTGCATTCATTTACGGCGGCG 367

     122 PheLeuPheSerLeuGluThrGlnThrThrIleGlyTyrGlyTyrArgCy 138
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     366 TTTTTATTCTCCCTTGAGACCCAAACCACCATCGGGTACGGTTACCGTTG 317

     138 sValThrGluGluCysSerValAlaValLeuMetValIleLeuGlnSerI 155
         |||||||||||||||||||||||||||||   |||||||||||||||||
     316 TGTCACGGAAGAATGCTCTGTGGCCGTGCTGACGGTCATCCTTCAGTCCA 267

     155 leLeuSerCysIleIleAsnThrPheIleIleGlyAlaAlaLeuAlaLys 171
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     266 TCCTGAGCTGCATCATAAACACCTTCATCATTGGGGCAGCCTTGGCAAAG 217

     172 MetAlaThrAlaArgLysArgAlaGlnThrIleArgPheSerTyrPheAl 188
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     216 ATGGCGACCGCCCGGAAGCGAGCCCAGACCATCCGCTTCAGCTATTTCGC 167

     188 aLeuIleGlyMetArgAspGlyLysLeuCysLeuMetTrpArgIleGlyA 205
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     166 ACTCATCGGCATGAGAGACGGGAAGCTTTGCCTCATGTGGCGCATAGGTG 117

     205 spPheArgProAsnHisValValGluGlyThrValArgAlaGlnLeuLeu 221
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     116 ACTTCCGACCCAACCATGTGGTGGAGGGCACGGTGAGAGCCCAACTTCTG 67

     222 ArgTyrThrGluAspSerGluGlyArgMetThrMetAlaPheLysAspLe 238
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seq_name: gb_est1:BB625105

seq_documentation_block:
LOCUS       BB625105                658 bp    mRNA    linear   EST 26-OCT-2001
DEFINITION  BB625105 RIKEN full-length enriched, adult male cecum Mus musculus
            cDNA clone 9130007L13 5', mRNA sequence.
ACCESSION   BB625105
VERSION     BB625105.1  GI:16463440
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 658)
  AUTHORS   Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A.
            , Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J., Konno,H., Kouda
            ,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M.,
            Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki
            ,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H.,
            Tagami,M., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toya,T.,
            Muramatsu,M. and Hayashizaki,Y.
  TITLE     RIKEN Mouse ESTs (Arakawa,T., et al. 2001)
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Yoshihide Hayashizaki
            Laboratory for Genome Exploration Research Group, RIKEN Genomic
            Sciences Center(GSC), Yokohama Institute
            The Institute of Physical and Chemical Research (RIKEN)
            1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
            Tel: 81-45-503-9222
            Fax: 81-45-503-9216
            Email: genome-res@gsc.riken.go.jp,
            URL:http://genome.gsc.riken.go.jp/
            Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
            ,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
             Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new
            genes. Genome Res. . 10 (10), 1617-1630 (2000)
             wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
            Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
            ,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
            Hayashizaki,Y.
             RIKEN integrated sequence analysis (RISA) system--384-format
            sequencing pipeline with 384 multicapillary sequencer. Genome Res. .
            10 (11), 1757-1771 (2000)
             Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara
            ,Y. and Hayashizaki,Y.
             Computer-based methods for the mouse full-length cDNA
            encyclopedia: real-time sequence clustering for construction of a
            nonredundant cDNA library. Genome Res. . 11 (2), 281-289 (2001)
             Kondo,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamanaka,I., Aizawa
            ,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and
            Hayashizaki,Y.
             Computational Analysis of Full-Length Mouse cDNAs Compared with
            Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
             Please visit our web site (http://genome.gsc.riken.go.jp) for
            further details.
             e mouse tissues.
FEATURES             Location/Qualifiers
     source          1. .658
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                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="9130007L13"
                     /clone_lib="RIKEN full-length enriched, adult male cecum"
                     /sex="male"
                     /tissue_type="cecum"
                     /dev_stage="adult"
                     /lab_host="DH10B"
                     /note="Site_1: SalI; Site_2: BamHI; cDNA library was
                     prepared and sequenced in Mouse Genome Encyclopedia
```

Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGAGAGAGAAGGATCCAAGAGCTCTTTTTTTTTTTTTTTVN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 10.0 and subtraction to Rot = 185.0. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGAGATTCTCGAGTTAATTAAATTAATCCCCCCCCCCCCC 3']. cDNA was cloned into the XhoI and BamHI sites. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I. Cloning sites, 5' end: SalI; 3' end: BamHI"

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ORIGIN

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Quality: 810.00 Length: 162
Ratio: 5.159 Gaps: 0
Percent Similarity: 96.914 Percent Identity: 91.358

alignment_block:
US-09-623-304A-1 x BB625105 ..

Align seg 1/1 to: BB625105 from: 1 to: 658

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        ||||||||||||||||||||||||||||||||||||||||||||||||||
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     51 PheGlyGluTrpGlySerTyrValValAspIlePheThrThrLeuValAs 67
        ||||||||||||||||||||||:::|||||||||||||||||||||||||
    320 TTTGGAGAATGGGGGAGCTACATGGTTGATATTTTTACCACTCTTGTGGA 369

     67 pThrLysTrpArgHisMetPheValIlePheSerLeuSerTyrIleLeuS 84
        ||||||||||||||||||||||||||||||||||||||||||||||||||
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        |||||||||:::|||||||||||||||||||||||||||||||||||||
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seq_name: gb_htc:AK017299

seq_documentation_block:

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DEFINITION  Mus musculus 6 days neonate head cDNA, RIKEN full-length enriched
            library, clone:5430411M10:potassium inwardly-rectifying channel,
            subfamily J, member 12, full insert sequence.
ACCESSION   AK017299
VERSION     AK017299.1  GI:12856469
KEYWORDS    HTC; CAP trapper.
SOURCE      Mus musculus (strain:C57BL/6J) 6 days neonate head cDNA to mRNA,
            clone_lib:RIKEN full-length enriched mouse cDNA library
            clone:5430411M10.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (sites)
  AUTHORS   Carninci,P. and Hayashizaki,Y.
  TITLE     High-efficiency full-length cDNA cloning
  JOURNAL   Meth. Enzymol. 303, 19-44 (1999)
  MEDLINE   99279253
   PUBMED   10349636
REFERENCE   2  (sites)
  AUTHORS   Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
            Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
  TITLE     Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new genes
  JOURNAL   Genome Res. 10 (10), 1617-1630 (2000)
  MEDLINE   20499374
   PUBMED   11042159
REFERENCE   3  (sites)
  AUTHORS   Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
            Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
            Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,
            Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,
            Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M.,
            Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J.,
            Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
  TITLE     RIKEN integrated sequence analysis (RISA) system--384-format
            sequencing pipeline with 384 multicapillary sequencer
  JOURNAL   Genome Res. 10 (11), 1757-1771 (2000)
  MEDLINE   20530913
   PUBMED   11076861
REFERENCE   4  (sites)
  AUTHORS   The RIKEN Genome Exploration Research Group Phase II Team and the
            FANTOM Consortium.
  TITLE     Functional annotation of a full-length mouse cDNA collection
  JOURNAL   Nature 409, 685-690 (2001)
REFERENCE   5  (bases 1 to 2462)
  AUTHORS   Adachi,J., Aizawa,K., Akahira,S., Akimura,T., Aono,H., Arai,A.,
            Arakawa,T., Baldarelli,R., Bono,H., Brownstein,M., Bult,C.,
            Carninci,P., Fukuda,S., Fukunishi,Y., Furuno,M., Hanagaki,T.,
            Hara,A., Hayatsu,N., Hill,D., Hiramoto,K., Hiraoka,T., Hori,F.,
            Hume,D., Imotani,K., Ishii,Y., Itoh,M., Izawa,M., Kasukawa,T.,
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            Saito,H., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D.,
            Schriml,L., Shibata,K., Shibata,Y., Shinagawa,A., Shiraki,T.,
            Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F.,
            Tanaka,T., Tejima,Y., Toya,T., Yamamura,T., Yamanaka,I.,
            Yasunishi,A., Yoshida,K., Yoshino,M., Muramatsu,M. and
            Hayashizaki,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of
            Physical and Chemical Research (RIKEN), Laboratory for Genome
            Exploration Research Group, RIKEN Gemomic Sciences Center (GSC),
            RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
            Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp,
            URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
            Fax:81-45-503-9216)
COMMENT     Please visit our web site (http://genome.gsc.riken.go.jp/) for
            further details.
            cDNA library was prepared and sequenced in Mouse Genome
            Encyclopedia Project of Genome Exploration Research Group in Riken
            Genomic Sciences Center and Genome Science Laboratory in RIKEN.
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          Division of Experimental Animal Research in Riken contributed to
          prepare mouse tissues. First strand cDNA was primed with a primer
          [5' GAGAGAGAGAAGGATCCAAGAGCTCTTTTTTTTTTTTTTTVN 3'], cDNA was
          prepared by using trehalose thermo-activated reverse transcriptase
          and subsequently enriched for full-length by cap-trapper. cDNA went
          through one round of normalization to Rot = 10.0 and subtraction to
          Rot = 100.0. Second strand cDNA was prepared with the primer
          adapter of sequence [5'
          GAGAGAGAGATTCTCGAGTTAATTAAATTAATCCCCCCCCCCCCCC 3']. cDNA was cleaved
          with BamHI and XhoI. Vector: a modified pBluescript KS(+) after
          bulk excision from Lambda FLC I. Cloning sites, 5' end: SalI; 3'
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ORIGIN


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    1225 GTCACAGAGGAGGGTGAG.................TACATCCCACTGGA 1256

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    1257 CCAGATTGACATCGATGTCGGCTTTGACAAGGGCCTAGACCGTATCTTCC 1306

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         |||||:::|||:::||||||:::||||||||||||:::   |||||||||
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     264 TyrAlaLeuAspArgLysAlaValAlaLysAspAsnPheGluIleLeuVa 280
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    1507 CTCTTCGAAGAGAAGAACCAGTACAAGATTGACTATTCACACTTCCACAA 1556

     330 ySerValGluVal...TyrAlaProPheCysSerAlaLysGlnLeu 344
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seq_documentation_block:
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DEFINITION  602105362F1 NCI_CGAP_Kid14 Mus musculus cDNA clone IMAGE:4223390
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ACCESSION   BF789809
VERSION     BF789809.1  GI:12094845
KEYWORDS    EST.
SOURCE      house mouse.
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REFERENCE   1  (bases 1 to 665)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Jeffrey E. Green, M.D.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM9811  row: l  column: 15
            High quality sequence stop: 617.
FEATURES             Location/Qualifiers
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                     /organism="Mus musculus"
                     /strain="FVB/N"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:4223390"
                     /clone_lib="NCI_CGAP_Kid14"
                     /lab_host="DH10B (T1 phage-resistant)"
                     /note="Organ: kidney; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally.  Primer: Oligo dT.
                     Average insert size 1.75 kb. Constructed by Life
                     Technologies. Note: this is a NCI_CGAP Library. |"
BASE COUNT      194 a    146 c    144 g    180 t      1 others
ORIGIN


alignment_scores:
            Quality:  792.50             Length:    179
              Ratio:  4.608                Gaps:      3
 Percent Similarity:  96.089   Percent Identity: 87.151

alignment_block:
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 Align seg 1/1  to: BF789809  from: 1  to: 665

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      17 rProGlyTyrProProGluHisIleIleAlaGluLysArgArgAlaArgA 34
         ||||||||||||||||||||   ||||||||||||||||||||||||||
     171 TCCAGGCTATCCTCCAGAGCATGCCATCGCTGAGAAGAGAAGAGCAAGAA 220

      34 rgArgLeuLeuHisLysAspGlySerCysAsnValTyrPheLysHisIle 50
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     221 GGCGCTTGCTCCACAAAGATGGCAGCTGTAATGTGTACTTTAAACACATT 270

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         ||||||||||||||||||||:::||||||||||||||||||||||||||
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      67 pThrLysTrpArgHisMetPheValIlePheSerLeuSerTyrIleLeuS 84
         ||||||||||||||||||||:::||||||||||||||||||||||||||
     321 TACCAAGTGGCGCCATATGTTCATAATATTTTCTCTGTCTTACATTCTCT 370

      84 erTrpLeuIlePheGlySerValPheTrpLeuIleAlaPheHisHisGly 100
         ||||||||||||||||||:::||||||||||||||||||||||||||||
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     101 AspLeuLeuAsnAspProAspIleThrProCysValAspAsnValHisSe 117
         |||||||||:::|||||||||||||||||||   ||||||||||||||
     421 GACCTATTAAGCGATCCAGATATCACCCCTTGTGT.GACAACGTGCATTC 469

     117 rPheThrGlyAlaPheLeuPheSerLeuGluThrGlnThrThrIleGlyT 134
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     150 lIleLeuGlnSerIleLeuSerCysIleIle.AsnThrPheIleIleGly 166
         ||||||||||||||||||||:::       :::|||||||||||||||||
     570 GATCCTTCAGTCCATCCTCAGTGCA...TCATAAAACCTTCATCATTGGA 616

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seq_name: gb_est1:BB643863

seq_documentation_block:
LOCUS       BB643863               641 bp    mRNA    linear   EST 31-AUG-2001
DEFINITION  BB643863 RIKEN full-length enriched, adult male corpora
            quadrigemina Mus musculus cDNA clone B230120P21 5', mRNA sequence.
ACCESSION   BB643863
VERSION     BB643863.1  GI:15402155
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 641)
  AUTHORS   Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A.
            , Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J., Konno,H., Kouda
            ,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M.,
            Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki
            ,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H.,
            Tagami,M., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toya,T.,
            Muramatsu,M. and Hayashizaki,Y.
  TITLE     RIKEN Mouse ESTs (Arakawa,T., et al. 2001)
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Yoshihide Hayashizaki
            Laboratory for Genome Exploration Research Group, RIKEN Genomic
            Sciences Center(GSC), Yokohama Institute
            The Institute of Physical and Chemical Research (RIKEN)
            1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
            Tel: 81-45-503-9222
            Fax: 81-45-503-9216
            Email: genome-res@gsc.riken.go.jp,
            URL:http://genome.gsc.riken.go.jp/
            Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
            ,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
             Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new
            genes. Genome Res. . 10 (10), 1617-1630 (2000)
             wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
            Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
            ,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
            Hayashizaki,Y.
             RIKEN integrated sequence analysis (RISA) system--384-format
            sequencing pipeline with 384 multicapillary sequencer. Genome Res. .
            10 (11), 1757-1771 (2000)
             Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara
            ,Y. and Hayashizaki,Y.
             Computer-based methods for the mouse full-length cDNA
            encyclopedia: real-time sequence clustering for construction of a
            nonredundant cDNA library. Genome Res. . 11 (2), 281-289 (2001)
             Yamanaka,I., Kiyosawa,H., Kondo,S., Saito,T., Shinagawa,A., Aizawa
            ,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K., Arakawa,T.,
            Ishii,Y. and Hayashizaki,Y.
             Mapping of 19032 mouse cDNAs on mouse chromosomes. J. Struct.
            Func. Genomics 2 pre, L72-L86 (2001
             Please visit our web site (http://genome.gsc.riken.go.jp) for
            further details.
             e mouse tissues.
FEATURES             Location/Qualifiers
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                     /dev_stage="adult"
                     /lab_host="DH10B"
                     /note="Site_1: SalI; Site_2: BamHI; cDNA library was
                     prepared and sequenced in Mouse Genome Encyclopedia
                     Project of Genome Exploration Research Group in Riken
                     Genomic Sciences Center and Genome Science Laboratory in
                     RIKEN. Division of Experimental Animal Research in Riken
                     contributed to prepare mouse tissues. 1st strand cDNA was
                     primed with a primer [5'
                     GAGAGAGAGAAGGATCCAAGAGCTCTTTTTTTTTTTTTTTVN 3'], cDNA was
                     prepared by using trehalose thermo-activated reverse
                     transcriptase and subsequently enriched for full-length by
                     cap-trapper. cDNA went through one round of normalization
                     to Rot = 20.0 and subtraction to Rot = 459.0. Second
                     strand cDNA was prepared with the primer adapter of
                     sequence [5' GAGAGAGAGATTCTCGAGTTAATTAAATTAATCCCCCCCCCCCCC
                     3']. cDNA was cleaved with XhoI and BamHI. Vector: a
                     modified pBluescript KS(+) after bulk excision from Lambda
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BASE COUNT      176 a    142 c    145 g    178 t
ORIGIN


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           Quality:  760.00            Length:    156
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 Percent Similarity:  95.513   Percent Identity: 89.744

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         ||||||||||||||||||||   ||||||||||||||||||||||||||
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         ||||||||||||||||||||||||||||||||||||||||||||||||||
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      67 pThrLysTrpArgHisMetPheValIlePheSerLeuSerTyrIleLeuS 84
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     372 TACCAAGTGGCGCCATATGTTCGTAATATTTTCTCTGTCTTACATTCTCT 421

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     101 AspLeuLeuAsnAspProAspIleThrProCysValAspAsnValHisSe 117
         |||||||||:::|||||||||||||||||||||||||||||||||||||||
     472 GACCTATTAAGCGATCCAGATATCACCCCTTGTGTTGACAACGTGCATTC 521

     117 rPheThrGlyAlaPheLeuPheSerLeuGluThrGlnThrThrIleGlyT 134
         |||||||:::|||||||||||||||||||||||||||||||||||||||||
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seq_name: gb_est1:AW475637

seq_documentation_block:
LOCUS       AW475637                721 bp    mRNA    linear   EST 24-FEB-2000
DEFINITION  un69d09.y1 Sugano mouse kidney mkia Mus musculus cDNA clone
            IMAGE:2520017 5' similar to TR:Q9Z307 Q9Z307 INWARDLY RECTIFYING
            POTASSIUM CHANNEL KIR5.1 ;, mRNA sequence.
ACCESSION   AW475637
VERSION     AW475637.1  GI:7045743
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
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            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 721)
  AUTHORS   Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T.,
            Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person
            ,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter
            ,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R.,
            Waterston,R. and Wilson,R.
  TITLE     The WashU-NCI Mouse EST Project 1999
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Marra M/WashU-NCI Mouse EST Project 1999
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: mouseest@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            MGI:1018741
            Trace considered overall poor quality
            Seq primer: custom primer used
            High quality sequence stop: 1.
FEATURES             Location/Qualifiers
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                     [ATGTGGCCTTTTTTTTTTTTTTT]; double-stranded cDNA was
                     ligated to a  DraIII adaptor [TGTTGGCCTACTGG], digested
                     and cloned into distinct DraIII sites of the pME18S-FL3
                     vector (5' site CACTGTGTG, 3' site CACCATGTG). XhoI should
                     be used to isolate the cDNA insert.  Size selection was
                     performed to exclude fragments <1.5kb.  Library
                     constructed by Dr. Sumio Sugano (University of Tokyo
                     Institute of Medical Science).  Custom primers  for
                     sequencing: 5' end primer CTTCTGCTCTAAAAGCTGCG and 3' end
                     primer CGACCTGCAGCTCGAGCACA."
BASE COUNT      208 a    176 c    179 g    158 t
ORIGIN


alignment_scores:
           Quality:  752.50            Length:    203
             Ratio:  4.300               Gaps:      1
 Percent Similarity:  86.207   Percent Identity: 74.384
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     197 uCysLeuMetTrpArgIleGlyAspPheArgProAsnHisValValGluG 214
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     214 lyThrValArgAlaGlnLeuLeuArgTyrThrGluAspSerGluGlyArg 230
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     455 AGCAGGGAATTCTACGCCCGCTTTGGCAGTGCCAAACAACTGGACTGTAA 504

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DEFINITION  BB644922 RIKEN full-length enriched, adult male corpora
            quadrigemina Mus musculus cDNA clone B230368J24 5', mRNA sequence.
ACCESSION   BB644922
VERSION     BB644922.1  GI:16479458
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
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            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 651)
  AUTHORS   Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A.
            , Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J., Konno,H., Kouda
            ,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M.,
            Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki
            ,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H.,
            Tagami,M., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toya,T.,
            Muramatsu,M. and Hayashizaki,Y.
  TITLE     RIKEN Mouse ESTs (Arakawa,T., et al. 2001)
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Yoshihide Hayashizaki
            Laboratory for Genome Exploration Research Group, RIKEN Genomic
            Sciences Center(GSC), Yokohama Institute
            The Institute of Physical and Chemical Research (RIKEN)
            1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
            Tel: 81-45-503-9222
            Fax: 81-45-503-9216
            Email: genome-res@gsc.riken.go.jp,
            URL:http://genome.gsc.riken.go.jp/
            Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
            ,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
             Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new
            genes. Genome Res. . 10 (10), 1617-1630 (2000)
             wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
            Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
            ,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
            Hayashizaki,Y.
             RIKEN integrated sequence analysis (RISA) system--384-format
            sequencing pipeline with 384 multicapillary sequencer. Genome Res. .
            10 (11), 1757-1771 (2000)
             Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara
            ,Y. and Hayashizaki,Y.
             Computer-based methods for the mouse full-length cDNA
            encyclopedia: real-time sequence clustering for construction of a
            nonredundant cDNA library. Genome Res. . 11 (2), 281-289 (2001)
             Kondo,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamanaka,I., Aizawa
            ,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and
            Hayashizaki,Y.
             Computational Analysis of Full-Length Mouse cDNAs Compared with
            Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
             Please visit our web site (http://genome.gsc.riken.go.jp) for
            further details.
             e mouse tissues.
FEATURES             Location/Qualifiers
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                     /dev_stage="adult"
                     /lab_host="DH10B"
                     /note="Site_1: SalI; Site_2: BamHI; cDNA library was
                     prepared and sequenced in Mouse Genome Encyclopedia
                     Project of Genome Exploration Research Group in Riken
                     Genomic Sciences Center and Genome Science Laboratory in
                     RIKEN. Division of Experimental Animal Research in Riken
                     contributed to prepare mouse tissues. 1st strand cDNA was
                     primed with a primer [5'
                     GAGAGAGAGAAGGATCCAAGAGCTCTTTTTTTTTTTTTTTVN 3'], cDNA was
                     prepared by using trehalose thermo-activated reverse
                     transcriptase and subsequently enriched for full-length by
                     cap-trapper. cDNA went through one round of normalization
                     to Rot = 20.0 and subtraction to Rot = 459.0. Second
                     strand cDNA was prepared with the primer adapter of
                     sequence [5' GAGAGAGAGATTCTCGAGTTAATTAAATTAATCCCCCCCCCCCCC
                     3']. cDNA was cleaved with XhoI and BamHI. Vector: a
                     modified pBluescript KS(+) after bulk excision from Lambda
                     FLC I."
BASE COUNT      179 a    136 c    150 g    186 t
ORIGIN
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      67 pThrLysTrpArgHisMetPheValIlePheSerLeuSerTyrIleLeuS 84
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     380 TACCAAGTGGCGCCATATGTTCGAAATATTTTCTCTGTCTTACATTCTCT 429

      84 erTrpLeuIlePheGlySerValPheTrpLeuIleAlaPheHisHisGly 100
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     430 CCTGGTTGATATTTGGCTCCATATTTTGGCTCATAGCCTTTCATCACGGA 479

     101 AspLeuLeuAsnAspProAspIleThrProCysValAspAsnValHisSe 117
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     480 GACCTATTAAGCGATCCAGATATTACCCCTTGTGTTGACAACGTGCATTC 529

     117 rPheThrGlyAlaPheLeuPheSerLeuGluThrGlnThrThrIleGlyT 134
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     530 ATTTACGGGTGCATTCTTATTCTCCCTGGAGACCCATACCACCATTGGAT 579

     134 yrGlyTyrArgCysValThrGluGluCys 143
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DEFINITION  602887019F1 NCI_CGAP_Kid14 Mus musculus cDNA clone IMAGE:5042285
            5', mRNA sequence.
ACCESSION   BI101289
VERSION     BI101289.1  GI:14552182
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 690)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Jeffrey E. Green, M.D.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM11116  row: e  column: 06
            High quality sequence start: 47
            High quality sequence stop: 651.
FEATURES             Location/Qualifiers
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                     Technologies. Note: this is a NCI_CGAP Library. |"
BASE COUNT      192 a    166 c    147 g    185 t
ORIGIN


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      17 yrProGlyTyrProProGluHisIleIleAlaGluLysArgArgAlaArg 33
         ||||||||||||||||||:::|||   ||||||||||||||||||||||
     196 ATCCAGGCTATCCTCCAGATCATGCCATCGCTGAGAAGAGAAGAGCAAGA 245

      34 ArgArgLeuLeuHisLysAspGlySerCysAsnValTyrPheLysHisIl 50
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      50 ePheGlyGluTrpGlySerTyrVal.ValAsp.IlePheThrThrLeuVa 66
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     296 TTTTGGAGAATGGGGGAGCTACATGGCTTGACTATTTTTACCACTCTTGT 345

      66 lAspThrLysTrpArgHisMetPheValIlePheSerLeuSerTyrIleL 83
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      83 euSerTrpLeuIlePheGlySerValPheTrpLeuIleAlaPheHisHis 99
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     396 TCTCCTGGTTGATATTTGGTTCCATATTTTGGCTCATAGCCTTTCATCAC 445

     100 GlyAspLeuLeuAsnAspProAspIleThrProCysValAspAsnValHi 116
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     116 sSerPheThrGlyAlaPheLeuPheSerLeuGlu.ThrGlnThrThrIle 132
         ||||||||||:::|||||||:::|||||||||||| ||||||:::||||||
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     133 GlyTyrGlyTyrArgCysValThr.GluGluCysSer.ValAlaValLeu 148
         |||||||||||||||||||||||| :::|||||||||| :::|||||||||
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     165 IleGlyAlaAlaLeuAlaLysMetAla 173
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Date: Aug 21, 2002 10:12 PM

About: Results were produced by the GenCore software, version 4.5,
       Copyright (c) 1993-2000 Compugen Ltd.

Command line parameters:
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 -TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct
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 -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
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Search information block:
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Query length: 383
Database: GenEmbl:*
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Database length: 1873333701
Search time (sec): 1882.350000


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gb_ov:GGU20216      +  840.00 1602.22  7.0e-81   2123  ! U20216 Gallus gallus inward re
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gb_ro:AB024304      +  837.50 1602.71  6.6e-81   1294  ! AB024304 Mus musculus mRNA for
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gb_om:AF021140      +  829.00 1586.27  5.4e-80   1284  ! AF021140 Sus scrofa inward rec
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gb_pr:HSU22413      +  827.00 1582.38  8.9e-80   1284  ! U22413 Human inward rectifi
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ACCESSION   AF179353
VERSION     AF179353.1  GI:9957531
KEYWORDS    .
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            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1257)
  AUTHORS   Liu,Y., McKenna,E., Figueroa,D.J., Blevins,R., Austin,C.P.,
            Bennett,P.B. and Swanson,R.
  TITLE     The human inward rectifier K+ channel subunit Kir5.1 maps to
            chromosome 17q25 and is expressed in kidney and pancreas
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 1257)
  AUTHORS   Liu,Y. and McKenna,E.
  TITLE     Direct Submission
  JOURNAL   Submitted (20-AUG-1999) Bioinformatics, Merck & Co., Inc.,
            WP42-300, West Point, PA 19486, USA
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 67 pThrLysTrpArgHisMetPheValIlePheSerLeuSerTyrIleLeuS 84
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 84 erTrpLeuIlePheGlySerValPheTrpLeuIleAlaPheHisHisGly 100
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167 aAlaLeuAlaLysMetAlaThrAlaArgLysArgAlaGlnThrIleArgP 184
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184 heSerTyrPheAlaLeuIleGlyMetArgAspGlyLysLeuCysLeuMet 200
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217 gAlaGlnLeuLeuArgTyrThrGluAspSerGluGlyArgMetThrMetA 234
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651 AGCCCAACTTCTCCGCTATACAGAAGACAGTGAAGGGAGGATGACGATGG 700

234 laPheLysAspLeuLysLeuValAsnAspGlnIleIleLeuValThrPro 250
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701 CATTTAAAGACCTCAAATTAGTCAACGACCAAATCATCCTGGTCACCCCG 750

251 ValThrIleValHisGluIleAspHisGluSerProLeuTyrAlaLeuAs 267
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267 pArgLysAlaValAlaLysAspAsnPheGluIleLeuValThrPheIleT 284
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317 sArgLysTyrTyrLysValAsnCysLeuGlnPheGluGlySerValGluV 334
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VERSION     AX179754.1  GI:15132118
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REFERENCE   1  (bases 1 to 1730)
  AUTHORS   Baughn,M.R., Burford,N., Au-Young,J., Lu,D.A., Yang,J., Reddy,R.,
            Lal,P., Hillman,J.L., Azimzai,Y., Yue,H., Nguyen,D.B., Yao,M.G.,
            Gandhi,A.R., Tang,Y.T. and Khan,F.A.
  TITLE     Transporters and ion channels
  JOURNAL   Patent: WO 0146258-A 42 28-JUN-2001;
            Incyte Genomics, Inc. (US)
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BASE COUNT      520 a    358 c    361 g    491 t
ORIGIN


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DEFINITION  Homo sapiens clone 3 inwardly-rectifying potassium channel Kir5.1
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ACCESSION   AF153817
VERSION     AF153817.1  GI:8132294
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1856)
  AUTHORS   Derst,C., Karschin,C., Wischmeyer,E., Hirsch,J.R.,
            Preisig-Muller,R., Rajan,S., Engel,H., Grzeschik,K., Daut,J. and
            Karschin,A.
  TITLE     Genetic and functional linkage of Kir5.1 and Kir2.1 channel
            subunits
  JOURNAL   FEBS Lett. 491 (3), 305-311 (2001)
   PUBMED   11240146
REFERENCE   2  (bases 1 to 1856)
  AUTHORS   Derst,C.
  TITLE     Direct Submission
  JOURNAL   Submitted (25-MAY-1999) Philipps University, Inst. f. Physiology,
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DEFINITION  Homo sapiens clone 1 inwardly-rectifying potassium channel Kir5.1
            (KCNJ16) mRNA, complete cds.
ACCESSION   AF153815
VERSION     AF153815.1  GI:8132290
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 2089)
  AUTHORS   Derst,C., Karschin,C., Wischmeyer,E., Hirsch,J.R.,
            Preisig-Muller,R., Rajan,S., Engel,H., Grzeschik,K., Daut,J. and
            Karschin,A.
  TITLE     Genetic and functional linkage of Kir5.1 and Kir2.1 channel
            subunits
  JOURNAL   FEBS Lett. 491 (3), 305-311 (2001)
   PUBMED   11240146
REFERENCE   2  (bases 1 to 2089)
  AUTHORS   Derst,C.
  TITLE     Direct Submission
  JOURNAL   Submitted (25-MAY-1999) Philipps University, Inst. f. Physiology,
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DEFINITION  Homo sapiens inwardly-rectifying potassium channel Kir5.1 (KCNJ16)
            gene, exon 5 and complete cds, alternatively spliced.
ACCESSION   AF153814
VERSION     AF153814.1  GI:8132310
KEYWORDS    .
SEGMENT     6 of 6
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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REFERENCE   1  (bases 1 to 3642)
  AUTHORS   Derst,C., Karschin,C., Wischmeyer,E., Hirsch,J.R.,
            Preisig-Muller,R., Rajan,S., Engel,H., Grzeschik,K., Daut,J. and
            Karschin,A.
  TITLE     Genetic and functional linkage of Kir5.1 and Kir2.1 channel
            subunits
  JOURNAL   FEBS Lett. 491 (3), 305-311 (2001)
   PUBMED   11240146
REFERENCE   2  (bases 1 to 3642)
  AUTHORS   Derst,C.
  TITLE     Direct Submission
  JOURNAL   Submitted (25-MAY-1999) Philipps University, Inst. f. Physiology,
            Deutschhausstr. 2, Marburg 35037, Germany
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ACCESSION   AF153816
VERSION     AF153816.1  GI:8132292
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REFERENCE   1  (bases 1 to 4021)
  AUTHORS   Derst,C., Karschin,C., Wischmeyer,E., Hirsch,J.R.,
            Preisig-Muller,R., Rajan,S., Engel,H., Grzeschik,K., Daut,J. and
            Karschin,A.
  TITLE     Genetic and functional linkage of Kir5.1 and Kir2.1 channel
            subunits
  JOURNAL   FEBS Lett. 491 (3), 305-311 (2001)
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  AUTHORS   Derst,C.
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  TITLE     Direct Submission
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            Deutschhausstr. 2, Marburg 35037, Germany
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DEFINITION  Homo sapiens chromosome 17, clone hRPK.1064_E_11, complete
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ACCESSION   AC005208
VERSION     AC005208.1  GI:3366585
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SOURCE      human.
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  AUTHORS   Birren,B., Linton,L., Nusbaum,C. and Lander,E.
  TITLE     Homo sapiens chromosome 17, clone hRPK.1064_E_11
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 123211)
  AUTHORS   Birren,B., Fasman,K., Linton,L., Nusbaum,C., Lander,E., Allen,N.,
            Baker,J., Baldwin,J., Barna,N., Beckerly,R., Benn,J., Boatin,C.,
            Boutwell,C., Brown,A., Castle,A., Cerny,J., Cooke,P., Depayre,E.,
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            Zody,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (30-JUN-1998) Whitehead Institute/MIT Center for Genome
            Research, 320 Charles Street, Cambridge, MA 02141, USA
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  AUTHORS   Birren,B., Fasman,K., Linton,L., Nusbaum,C., Lander,E., Allen,N.,
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  TITLE     Direct Submission
  JOURNAL   Submitted (29-JUL-1998) Whitehead Institute/MIT Center for Genome
            Research, 320 Charles Street, Cambridge, MA 02141, USA
REFERENCE   4  (bases 1 to 123211)
  AUTHORS   Birren,B., Fasman,K., Linton,L., Nusbaum,C., Lander,E., Allen,N.,
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  TITLE     Direct Submission
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            Research, 320 Charles Street, Cambridge, MA 02141, USA
COMMENT     On Jul 31, 1998 this sequence version replaced gi:3347827.
            All repeats were identified using RepeatMasker: Smit, A.F.A. &
            Green, P. (1996-1997)
            http://ftp.genome.washington.edu/RM/RepeatMasker.html

            Only the first 123.2 kilobases of this clone are being submitted.
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alignment_block:
 US-09-623-304A-1 x AC005208   ..

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      17 rProGlyTyrProProGluHisIleIleAlaGluLysArgArgAlaArgA 34
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  107334 CCCAGGCTACCCGCCAGAGCACATTATAGCTGAGAAGAGAAGAGCAAGAA 107383

      34 rgArgLeuLeuHisLysAspGlySerCysAsnValTyrPheLysHisIle 50
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      51 PheGlyGluTrpGlySerTyrValValAspIlePheThrThrLeuValAs 67
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  107434 TTTGGAGAATGGGGAAGCTATGTGGTTGACATCTTCACCACTCTTGTGGA 107483

      67 pThrLysTrpArgHisMetPheValIlePheSerLeuSerTyrIleLeuS 84
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  107484 CACCAAGTGGCGCCATATGTTTGTGATATTTTCTTTATCTTATATTCTCT 107533

      84 erTrpLeuIlePheGlySerValPheTrpLeuIleAlaPheHisHisGly 100
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  107534 CGTGGTTGATATTTGGCTCTGTCTTTTGGCTCATAGCCTTTCATCATGGC 107583

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     117 rPheThrGlyAlaPheLeuPheSerLeuGluThrGlnThrThrIleGlyT 134
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  107734 ATCCTCCAGTCCATCTTAAGTTGCATCATAAATACCTTTATCATTGGAGC 107783

     167 aAlaLeuAlaLysMetAlaThrAlaArgLysArgAlaGlnThrIleArgP 184
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     184 heSerTyrPheAlaLeuIleGlyMetArgAspGlyLysLeuCysLeuMet 200
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  107834 TCAGCTACTTTGCACTTATAGGTATGAGAGATGGGAAGCTTTGCCTCATG 107883

     201 TrpArgIleGlyAspPheArgProAsnHisValValGluGlyThrValAr 217
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  107884 TGGCGCATTGGTGATTTTCGGCCAAACCACGTGGTAGAAGGAACAGTTAG 107933

     217 gAlaGlnLeuLeuArgTyrThrGluAspSerGluGlyArgMetThrMetA 234
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  107934 AGCCCAACTTCTCCGCTATACAGAAGACAGTGAAGGGAGGATGACGATGG 107983

     234 laPheLysAspLeuLysLeuValAsnAspGlnIleIleLeuValThrPro 250
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     251 ValThrIleValHisGluIleAspHisGluSerProLeuTyrAlaLeuAs 267
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     267 pArgLysAlaValAlaLysAspAsnPheGluIleLeuValThrPheIleT 284
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     317 sArgLysTyrTyrLysValAsnCysLeuGlnPheGluGlySerValGluV 334
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     334 alTyrAlaProPheCysSerAlaLysGlnLeuAspTrpLysAspGlnGln 350
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     351 LeuHisIleGluLysAlaProProValArgGluSerCysThrSerAspTh 367
         ||||||||||||||||||||||||||||||||||||||||||||||||||
  108334 CTCCACATAGAAAAAGCACCACCAGTTCGAGAATCCTGCACGTCGGACAC 108383

     367 rLysAlaArgArgArgSerPheSerAlaValAlaIleValSerSer 382
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seq_name: gb_htg:AL662912

seq_documentation_block:
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DEFINITION  Mus musculus chromosome 11 clone RP23-408D5, *** SEQUENCING IN
            PROGRESS ***, in unordered pieces.
ACCESSION   AL662912
VERSION     AL662912.10  GI:18477421
KEYWORDS    HTG; HTGS_PHASE1; HTGS_ACTIVEFIN; HTGS_DRAFT; HTGS_FULLTOP.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (sites)
  AUTHORS   Tracey,A.
  TITLE     Direct Submission
  JOURNAL   Submitted (30-JAN-2002) Wellcome Trust Sanger Institute, Hinxton,
            Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
            humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
COMMENT     On Feb 1, 2002 this sequence version replaced gi:18476962.
            -------------- Genome Center
            Center: Wellcome Trust Sanger Institute
            Center code: SC
            Web site: http://www.sanger.ac.uk
            Contact: humquery@sanger.ac.uk
            -------------- Project Information
            Center project name: bM408D5
            -------------- Summary Statistics
            Assembly program: XGAP4; version 4.5
            Sequencing vector: plasmid; L08752; 100% of reads
            Chemistry: Dye-terminator Big Dye; 100% of reads
            Consensus quality: 193498 bases at least Q40
            Consensus quality: 193567 bases at least Q30
            Consensus quality: 193654 bases at least Q20
            Insert size: 193741; sum-of-contigs
            Insert size: 190800; 1.9% error; agarose-fp
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            coverage: 11.24x in Q20 bases; agarose-fp
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            * NOTE: This is a 'working draft' sequence.
            * This record will be updated with the finished sequence
            * as soon as it is available and the accession number will
            * be preserved.
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     misc_feature    122856. .150373
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     misc_feature    150474. .180083
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BASE COUNT    57238 a  38907 c  39270 g  58326 t    300 others
ORIGIN


alignment_scores:
            Quality: 1901.50            Length:    383
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                Ratio:  5.044              Gaps:      1
  Percent Similarity:  98.433   Percent Identity: 93.473

alignment_block:
 US-09-623-304A-1 x AL662912   ..

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      17 rProGlyTyrProProGluHisIleIleAlaGluLysArgArgAlaArgA 34
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   77026 TCCAGGCTATCCTCCAGAGCATGCCATCGCTGAGAAGAGAAGAGCAAGAA 77075

      34 rgArgLeuLeuHisLysAspGlySerCysAsnValTyrPheLysHisIle 50
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   77126 TTTGGAGAATGGGGGAGCTACATGGTTGATATTTTTACCACTCTTGTGGA 77175

      67 pThrLysTrpArgHisMetPheValIlePheSerLeuSerTyrIleLeuS 84
         ||||||||||||||||||||||||||||||||||||||||||||||||||
   77176 TACCAAGTGGCGCCATATGTTCGTAATATTTTCTCTGTCTTACATTCTCT 77225

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   77226 CCTGGTTGATATTTGGCTCCATATTTTGGCTCATAGCCTTTCATCACGGA 77275

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     134 yrGlyTyrArgCysValThrGluGluCysSerValAlaValLeuMetVal 150
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   77376 ACGGTTACCGCTGTGTCACCGAAGAGTGCTCTGTGGCTGTACTGACAGTG 77425

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     167 aAlaLeuAlaLysMetAlaThrAlaArgLysArgAlaGlnThrIleArgP 184
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   77476 AGCCTTGGCAAAGATGGCAACTGCCCGGAAGAGAGCCCAGACCATACGCT 77525

     184 heSerTyrPheAlaLeuIleGlyMetArgAspGlyLysLeuCysLeuMet 200
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   77526 TCAGCTATTTTGCCCTCATTGGTATGAGAGACGGGAAGCTTTGCCTCATG 77575

     201 TrpArgIleGlyAspPheArgProAsnHisValValGluGlyThrValAr 217
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   77576 TGGCGCATAGGTGACTTCCGACCAAACCATGTGGTAGAGGGCACGGTGAG 77625

     217 gAlaGlnLeuLeuArgTyrThrGluAspSerGluGlyArgMetThrMetA 234
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   77626 AGCCCAACTTCTGCGCTATTCAGAAGACAGTGAAGGGAGGATGACGATGG 77675

     234 laPheLysAspLeuLysLeuValAsnAspGlnIleIleLeuValThrPro 250
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     251 ValThrIleValHisGluIleAspHisGluSerProLeuTyrAlaLeuAs 267
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     267 pArgLysAlaValAlaLysAspAsnPheGluIleLeuValThrPheIleT 284
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      301 ProArg***IleLeuTrpGlyHisArgPheAsnAspValLeuGluValLy 317
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      317 sArgLysTyrTyrLysValAsnCysLeuGlnPheGluGlySerValGluV 334
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    77926 GAGAAAGTACTACAAGGTGAACTGCTTGCAGTTTGAAGGAAGCGTGGAAG 77975

      334 alTyrAlaProPheCysSerAlaLysGlnLeuAspTrpLysAspGlnGln 350
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    77976 TCTACGCCCCCTTTTGCAGTGCCAAACAACTGGACTGGAAGGACCAACAA 78025

      351 Leu...HisIleGluLysAlaProProValArgGluSerCysThrSerAs 366
          |||   ::::::||||||:::   |||:::|||   ||||||:::|||||
    78026 CTCAACAACTTGGAGAAAACGTCCCCTGCCCGAGGATCCTGCAATTCTGA 78075

      366 pThrLysAlaArgArgArgSerPheSerAlaValAlaIleValSerSer 382
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seq_name: gb_htg:AL592422

seq_documentation_block:
LOCUS       AL592422              205947 bp    DNA     linear   HTG 06-DEC-2001
DEFINITION  Mus musculus chromosome 11 clone RP23-218O16, *** SEQUENCING IN
            PROGRESS ***, in unordered pieces.
ACCESSION   AL592422
VERSION     AL592422.10  GI:17426517
KEYWORDS    HTG; HTGS_PHASE1; HTGS_ACTIVEFIN; HTGS_DRAFT; HTGS_FULLTOP.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (sites)
  AUTHORS   Almeida,J.
  TITLE     Direct Submission
  JOURNAL   Submitted (05-DEC-2001) Wellcome Trust Sanger Institute, Hinxton,
            Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
            humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
COMMENT     On Dec 8, 2001 this sequence version replaced gi:17148386.
            -------------- Genome Center
            Center: Wellcome Trust Sanger Institute
            Center code: SC
            Web site: http://www.sanger.ac.uk
            Contact: humquery@sanger.ac.uk
            -------------- Project Information
            Center project name: bM218O16
            -------------- Summary Statistics
            Assembly program: XGAP4; version 4.5
            Sequencing vector: plasmid; L08752; 100% of reads
            Chemistry: Dye-terminator Big Dye; 100% of reads
            Consensus quality: 205509 bases at least Q40
            Consensus quality: 205628 bases at least Q30
            Consensus quality: 205703 bases at least Q20
            Insert size: 205747; sum-of-contigs
            Insert size: 189076; 6.5% error; agarose-fp
            Quality coverage: 11.16x in Q20 bases; sum-of-contigs Quality
            coverage: 12.15x in Q20 bases; agarose-fp
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            * NOTE: This is a 'working draft' sequence.
            * This record will be updated with the finished sequence
            * as soon as it is available and the accession number will
            * be preserved.
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BASE COUNT    60154 a  41276 c  41689 g  62628 t    200 others
ORIGIN


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            Quality: 1901.50              Length:    383
              Ratio:  5.044                Gaps:      1
 Percent Similarity:  98.433   Percent Identity: 93.473

alignment_block:
 US-09-623-304A-1 x AL592422   ..

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      17 rProGlyTyrProProGluHisIleIleAlaGluLysArgArgAlaArgA 34
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  162793 TCCAGGCTATCCTCCAGAGCATGCCATCGCTGAGAAGAGAAGAGCAAGAA 162842

      34 rgArgLeuLeuHisLysAspGlySerCysAsnValTyrPheLysHisIle 50
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  162843 GGCGCTTGCTCCACAAAGATGGCAGCTGTAATGTGTACTTTAAACACATT 162892

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     151 IleLeuGlnSerIleLeuSerCysIleIleAsnThrPheIleIleGlyAl 167
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DEFINITION  Rattus norvegicus Kir5.1 (kcnj16) gene, complete cds.
ACCESSION   AF249676
VERSION     AF249676.1  GI:8272583
KEYWORDS    .
SOURCE      Norway rat.
  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
REFERENCE   1  (bases 1 to 1260)
  AUTHORS   Tucker,S.J., Imbrici,P., Salvatore,L., D'Adamo,M.C. and Pessia,M.
  TITLE     pH dependence of the inwardly rectifying potassium channel, Kir5.1,
            and localization in renal tubular epithelia
  JOURNAL   J. Biol. Chem. 275 (22), 16404-16407 (2000)
  MEDLINE   20287495
REFERENCE   2  (bases 1 to 1260)
  AUTHORS   Tucker,S.J. and Pessia,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-MAR-2000) University Laboratory of Physiology, Oxford
            University, Parks Road, Oxford, Oxon OX1 3PT, United Kingdom
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DEFINITION  Mus musculus Kcnj16 mRNA for inwardly rectifying potassium channel
            Kir5.1, partial cds.
ACCESSION   AB016197
VERSION     AB016197.1  GI:3953532
KEYWORDS    inwardly rectifying potassium channel Kir5.1.
SOURCE      Mus musculus (strain:C57) 19 weeks old females brain cDNA to mRNA.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 1257)
  AUTHORS   Horio,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (11-JUL-1998) Yoshiyuki Horio, Faculty of Medicine, Osaka
            University, Department of Pharmacology II; 2-2 Yamadaoka, Suita,
            Osaka 565-0871, Japan (E-mail:horio@pharma2.med.osaka-u.ac.jp,
            Tel:81-6-879-3512, Fax:81-6-879-3519)
REFERENCE   2  (sites)
  AUTHORS   Mouri,T., Kittaka,N., Horio,Y., Copeland,N.G., Gilbert,D.J.,
            Jenkins,N.A. and Kurachi,Y.
  TITLE     Assignment of mouse inwardly rectifying potassium channel Kcnj16 to
            the distal region of mouse chromosome 11
  JOURNAL   Genomics 54 (1), 181-182 (1998)
  MEDLINE   99026146
COMMENT     On Dec 3, 1998 this sequence version replaced gi:3928763.
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DEFINITION  R.rattus mRNA for inward rectifier 9.
ACCESSION   X83581
VERSION     X83581.1  GI:609671
KEYWORDS    inward rectifier potassium channel.
SOURCE      black rat.
  ORGANISM  Rattus rattus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
REFERENCE   1  (bases 1 to 1155)
  AUTHORS   Bond,C.T., Pessia,M., Xia,X.M., Lagrutta,A., Kavanaugh,M.P. and
            Adelman,J.P.
  TITLE     Cloning and expression of a family of inward rectifier potassium
            channels
  JOURNAL   Recept. Channels 2 (3), 183-191 (1994)
  MEDLINE   95179470
  REMARK    Erratum:[[published erratum appears in Receptors Channels
            1994;2(4):following 350]]
REFERENCE   2  (bases 1 to 1155)
  AUTHORS   Adelman,J.P.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-DEC-1994) J.P. Adelman, Vollum Insitute for Advanced
            Biomedical, Research (VIABR), Oregon Health Sciences Univeristy,
            L474, 3181 SW Sam Jackson Park Rd., Portland OR 97201, USA
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BASE COUNT      294 a    295 c    291 g    275 t
ORIGIN


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              Ratio:  5.001               Gaps:      2
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      17 rProGlyTyrProProGluHisIleIleAlaGluLysArgArgAlaArgA 34
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      51 TCCAGGCTATCCTCCAGAGCATGCCATAGCCGAGAAGAGAAGAGCGAGGA 100

      34 rgArgLeuLeuHisLysAspGlySerCysAsnValTyrPheLysHisIle 50
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301 GACCTATTAAGCGATCCAGACATCACCCCGTGCGTGGACAACGTGCATTC 350

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134 yrGlyTyrArgCysValThrGluGluCysSerValAlaValLeuMetVal 150
401 ACGGTTACCGTTGTGTCACGGAAGAATGCTCTGTGGCCGTGCTGACGGTC 450

151 IleLeuGlnSerIleLeuSerCysIleIleAsnThrPheIleIleGlyAl 167
451 ATCCTTCAGTCCATCCTGAGCTGCATCATAAACACCTTCATCATTGGGGC 500

167 aAlaLeuAlaLysMetAlaThrAlaArgLysArgAlaGlnThrIleArgP 184
501 AGCCTTGGCAAAGATGGCGACCGCCCGGAAGCGAGCCCAGACCATCCGCT 550

184 heSerTyrPheAlaLeuIleGlyMetArgAspGlyLysLeuCysLeuMet 200
551 TCAGCTATTTCGCACTCATCGGCATGAGAGACGGGAAGCTTTGCCTCATG 600

201 TrpArgIleGlyAspPheArgProAsnHisValValGluGlyThrValAr 217
601 TGGCGCATAGGTGACTTCCGACCGAACCATGTGGTGGAGGGCACGGTGAG 650

217 gAlaGlnLeuLeuArgTyrThrGluAspSerGluGlyArgMetThrMetA 234
651 AGCCCAACTTCTGCGCTATTCAGAAGACAGCGAAGGGCGGATGACGATGG 700

234 laPheLysAspLeuLysLeuValAsnAspGlnIleIleLeuValThrPro 250
701 CGTTTAAAGACCTCAAACTCGTCAATGACCAGATAATCCTGGTAACGCCA 750

251 ValThrIleValHisGluIleAspHisGluSerProLeuTyrAlaLeuAs 267
751 GTGACCATTGTCCATGAAATTGACCACGAGAGTCCTCTGTATGCCCTTGA 800

267 pArgLysAlaValAlaLysAspAsnPheGluIleLeuValThrPheIleT 284
801 CCGCAAGGCAGTGGCCAAAGATAATTTCGAGATTCTGGTGACATTTATTT 850

284 yrThrGlyAspSerThrGlyThrSerHisGlnSerArgSerSerTyrVal 300
851 ATACTGGTGACTCTACTGGGACATCCCACCAGTCCAGAAGTTCCTACGTC 900

301 ProArg***IleLeuTrpGlyHisArgPheAsnAspValLeuGluValLy 317
901 CCCAGAGAAATTCTCTGGGGACACAGGTTTCATGATGTATTGGAAGTGAA 950

317 sArgLysTyrTyrLysValAsnCysLeuGlnPheGluGlySerValGluV 334
951 GAGAAAGTACTACAAGGTAAACTGCTTGCAGTTTGAGGGAAGCGTGGAAG 1000

334 alTyrAlaProPheCysSerAlaLysGlnLeuAspTrpLysAspGlnGln 350
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1051 CTCAACAACTTGGAGAAAACGTCCCCTGCGCCGAGGATCCTGCACCTCGG 1100

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seq_documentation_block:
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DEFINITION  Mus musculus clone RP23-320C8, WORKING DRAFT SEQUENCE, 7 unordered
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ACCESSION   AC025586
VERSION     AC025586.3  GI:9972313
KEYWORDS    HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 187774)
  AUTHORS   McCombie,W.R., Baker,J.P., Bahret,A., Bal,H., Dedhia,N.N., de la
            Bastide,M., Huang,E.N., King,L., Kirchoff,K.A., Miller,B.,
            Nascimento,L.U., O'Shaughnessy,A.L., Preston,R.R., Rodriguez,M.A.,
            Shah,R.S., Shekher,M., Spiegel,L.A., Toth,K. and Vil,M.D.
  TITLE     Mouse Genomic Sequence
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 187774)
  AUTHORS   McCombie,W.R.
  TITLE     Direct Submission
  JOURNAL   Submitted (13-MAR-2000) Lita Annenberg Hazen Genome Sequencing
            Center, Cold Spring Harbor Laboratory, 1 Bungtown Road, Cold Spring
            Harbor, NY 11724, USA
COMMENT     On Sep 6, 2000 this sequence version replaced gi:8439867.
            ------------------- Genome Center
            Center: Lita Annenberg Hazen Genome Center, Cold Spring Harbor
            Laboratory
            Center code: CSHL
            Web site: http://www.cshl.org/genseq
            Contact:  mccombie@cshl.org
            ------------------- Project Information
            Center project name: RP23-320C8
            Center clone name: RP23-320C8
            -------------------.
            * NOTE: This is a 'working draft' sequence. It currently
            * consists of 7 contigs. The true order of the pieces
            * is not known and their order in this sequence record is
            * arbitrary. Gaps between the contigs are represented as
            * runs of N, but the exact sizes of the gaps are unknown.
            * This record will be updated with the finished sequence
            * as soon as it is available and the accession number will
            * be preserved.
            *        1    62545: contig of 62545 bp in length
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            *    62976   123025: contig of 60050 bp in length
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            *   145176   145604: gap of unknown length
            *   145605   166987: contig of 21383 bp in length
            *   166988   167416: gap of unknown length
            *   167417   180022: contig of 12606 bp in length
            *   180023   180451: gap of unknown length
            *   180452   184785: contig of 4334 bp in length
            *   184786   185214: gap of unknown length
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DEFINITION  Anguilla japonica mRNA for eKir, complete cds.
ACCESSION   AB009669
VERSION     AB009669.1  GI:4630767
KEYWORDS    eKir.
SOURCE      Anguilla japonica cDNA to mRNA.
  ORGANISM  Anguilla japonica
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Anguilliformes;
            Anguillidae; Anguilla.
REFERENCE   1  (sites)
  AUTHORS   Suzuki,Y., Itakura,M., Kashiwagi,M., Nakamura,N., Matsuki,T.,
            Sakuta,H., Naito,N., Takano,K., Fujita,T. and Hirose,S.
  TITLE     Identification by differential display of a hypertonicity-inducible
            inward rectifier potassium channel highly expressed in chloride
            cells
  JOURNAL   J. Biol. Chem. 274 (16), 11376-11382 (1999)
  MEDLINE   99214223
REFERENCE   2  (bases 1 to 1119)
  AUTHORS   Suzuki,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (11-DEC-1997) Yoshiro Suzuki, Tokyo Institute of
            Technology, Department of Biological Sciences; 4259 Nagatsuta-cho,
            Midori-ku, Yokohama, Kanagawa 226-8501, Japan
            (E-mail:yosuzuki@bio.titech.ac.jp, Tel:81-45-924-5726,
            Fax:81-45-924-5824)
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ORIGIN


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     218 laGlnLeuLeuArgTyrThrGluAspSerGluGlyArgMetThrMetAla 234
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     235 PheLysAspLeuLysLeuValAsnAspGlnIleIleLeuValThrProVa 251
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     268 rgLysAlaValAlaLysAspAsnPheGluIleLeuValThrPheIleTyr 284
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ACCESSION   AF021141
VERSION     AF021141.1  GI:2460311
KEYWORDS    .
SOURCE      chicken.
  ORGANISM  Gallus gallus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
            Phasianinae; Gallus.
REFERENCE   1  (bases 1 to 1284)
  AUTHORS   Rae,J.L. and Shepard,A.R.
  TITLE     Inwardly rectifying potassium channels in lens epithelium are from
            the IRK1 (Kir 2.1) family
  JOURNAL   Exp. Eye Res. 66 (3), 347-359 (1998)
  MEDLINE   98288410
   PUBMED   9533862
REFERENCE   2  (bases 1 to 1284)
  AUTHORS   Rae,J.L. and Shepard,A.R.
  TITLE     Direct Submission
  JOURNAL   Submitted (28-AUG-1997) Physiology and Biophysics, Mayo Foundation,
            200 1st Street SW, Rochester, MN 55905, USA
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ORIGIN


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Date: Aug 21, 2002 10:17 PM

About: Results were produced by the GenCore software, version 4.5,
Copyright (c) 1993-2000 Compugen Ltd.

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Database: N_Geneseq_032802:*
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AC   AAZ21041;
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DT   01-DEC-1999  (first entry)
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DE   Human Kir5.1 inward rectifier potassium channel alpha subunit cDNA.
XX
KW   Potassium channel; inward rectifier; hypertension; renal failure;
KW   diabetes; cystic fibrosis; hypothyroidism; hyperthyroidism; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
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XX
PA   (ICAG-) ICAGEN INC.
XX
PI   Silvia C,  Yu W;
XX
DR   WPI; 1999-551066/46.
DR   P-PSDB; AAY42260.
XX
PT   A new potassium channel alpha subunit, Kir5.1, useful for treating
PT   hypertension, acute or chronic renal failure, diabetes insipidus or
PT   nephropathy -
XX
PS   Claim 4; Page 64-65; 68pp; English.
XX
CC   This sequence represents a human Kir5.1 inward rectifier potassium
CC   channel alpha subunit cDNA. This was isolated and amplified from a human
CC   testis cDNA library using PCR primers AAZ21042 and AAZ21043. The Kir5.1
CC   alpha subunit is predicted to be approximately 43 kD. The C-terminal
CC   tail region (residues 352-383) is divergent with respect to Kir5.1
CC   proteins from other species - for example, there is only 10% identity
CC   between the Kir5.1 tail regions of human and rat. Potassium channels are
CC   typically formed by four alpha subunits, each with two transmembrane
CC   domains, and can be homomeric (made of identical subunits) or heteromeric
CC   (made of two or more distinct types of alpha subunits). The human Kir5.1
CC   alpha subunit associates with additional alpha subunits to form a
CC   potassium channel which allows potassium influx to a cell, with little
CC   potassium outflux (inward rectifier activity). Such inward rectifier
CC   potassium channels comprising human Kir5.1 can be heteromeric, containing
CC   one or more Kir5.1 alpha subunits, along with other alpha subunits from
CC   the Kir family. Kir5.1 can also comprise a homomeric inward rectifier
CC   channel. The cDNA can be used to screen for modulators of inward
CC   rectifier potassium channels that contain a Kir5.1 subunit, for the
CC   treatment of hypertension, acute or chronic renal failure, diabetes
CC   insipidus or diabetic nephropathy, hypo- or hyperthyroidism, goitre,
CC   hypo- or hyperparathyroidism, pancreatic insufficiency, diabetes, cystic
CC   fibrosis, sialorrhoea, and salivary insufficiency.
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              Ratio:  5.293                Gaps:      0
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      67 pThrLysTrpArgHisMetPheValIlePheSerLeuSerTyrIleLeuS 84
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      84 erTrpLeuIlePheGlySerValPheTrpLeuIleAlaPheHisHisGly 100
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         ||||||||||||||||||||||||||||||||||||||||||||||||||
    1046 TATATGCCCCCTTTTGCAGTGCCAAGCAATTGGACTGGAAAGACCAGCAG 1095

     351 LeuHisIleGluLysAlaProProValArgGluSerCysThrSerAspTh 367
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    1096 CTCCACATAGAAAAAGCACCACCAGTTCGAGAATCCTGCACGTCGGACAC 1145

     367 rLysAlaArgArgArgSerPheSerAlaValAlaIleValSerSerTrp 383
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    1146 CAAGGCGAGACGAAGGTCATTTAGTGCAGTTGCCATTGTCAGCAGCTGG 1194

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seq_documentation_block:
ID   AAF85049 standard; DNA; 1257 BP.
XX
AC   AAF85049;
XX
DT   09-JUL-2001  (first entry)
XX
DE   Nucleotide sequence of a human Kir5.1 polypeptide.
XX
KW   Kir5.1; inwardly rectifying potassium channel; ion channel;
KW   renal failure; hypokalemia; hypertension; hypotension; thyroid disease;
KW   pancreatitis; ss.
XX
OS   Homo sapiens.
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FH   Key             Location/Qualifiers
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FT                   /*tag=  a
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XX
PN   WO200125258-A1.
XX
PD   12-APR-2001.
XX
PF   29-SEP-2000; 2000WO-US26996.
XX
PR   04-OCT-1999;   99US-0157491.
XX
PA   (MERI ) MERCK & CO INC.
XX
PI   Swanson RJ,  Liu Y,  McKenna E;
XX
DR   WPI; 2001-290604/30.
DR   P-PSDB; AAB68275.
XX
PT   Novel nucleic acid encoding human Kir5.1 subunit protein useful for
PT   identifying activators and inhibitors of potassium channels containing
PT   the protein subunit useful for treating various diseases  -
```

```
XX
PS   Claim 3; Fig 1; 52pp; English.
XX
CC   The present sequence encodes a human Kir5.1 subunit protein. Kir5.1
CC   is an inwardly rectifying potassium channel subunit. Kir5.1 proteins
CC   are useful for identifying inhibitors or activators of potassium
CC   channels. Kir5.1 proteins are useful as attractive targets for drug
CC   discovery and as valuable research tools for understanding ion channel
CC   biology. Kir5.1 proteins are also useful for identifying inhibitors or
CC   activators of potassium channels. Inhibitors or activators screened
CC   using Kir5.1 protein are useful for treating a variety of diseases
CC   involving excessive or insufficient potassium channel activity, such as
CC   renal failure, hypokalemia, hypertension, hypotension, thyroid disease
CC   and pancreatitis.
XX
SQ   Sequence 1257 BP; 358 A; 287 C; 276 G; 336 T; 0 other;


alignment_scores:
            Quality: 2011.00              Length:    382
              Ratio:  5.278                Gaps:      0
 Percent Similarity:  99.738   Percent Identity: 99.738

alignment_block:
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      17 rProGlyTyrProProGluHisIleIleAlaGluLysArgArgAlaArgA 34
         ||||||||||||||||||||||||||||||||||||||||||||||||||
      51 CCCAGGCTACCCGCCAGAGCACATTATAGCTGAGAAGAGAAGAGCAAGAA 100

      34 rgArgLeuLeuHisLysAspGlySerCysAsnValTyrPheLysHisIle 50
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     101 GACGATTACTTCACAAAGATGGCAGCTGTAATGTCTACTTCAAGCACATT 150

      51 PheGlyGluTrpGlySerTyrValValAspIlePheThrThrLeuValAs 67
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     151 TTTGGAGAATGGGGAAGCTATGTGGTTGACATCTTCACCACTCTTGTGGA 200

      67 pThrLysTrpArgHisMetPheValIlePheSerLeuSerTyrIleLeuS 84
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     201 CACCAAGTGGCGCCATATGTTTGTGATATTTTCTTTATCTTATATTCTCT 250

      84 erTrpLeuIlePheGlySerValPheTrpLeuIleAlaPheHisHisGly 100
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     251 CGTGGTTGATATTTGGCTCTGTCTTTTGGCTCATAGCCTTTCATCATGGC 300

     101 AspLeuLeuAsnAspProAspIleThrProCysValAspAsnValHisSe 117
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     301 GATCTATTAAATGATCCAGACATCACACCTTGTGTTGACAACGTCCATTC 350

     117 rPheThrGlyAlaPheLeuPheSerLeuGluThrGlnThrThrIleGlyT 134
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     351 TTTCACAGGGGCCTTTTTGTTCTCCCTAGAGACCCAAACCACCATAGGAT 400

     134 yrGlyTyrArgCysValThrGluGluCysSerValAlaValLeuMetVal 150
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     401 ATGGTTATCGCTGTGTTACTGAAGAATGTTCTGTGGCCGTGCTCATGGTG 450

     151 IleLeuGlnSerIleLeuSerCysIleIleAsnThrPheIleIleGlyAl 167
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     451 ATCCTCCAGTCCATCTTAAGTTGCATCATAAATACCTTTATCATTGGAGC 500

     167 aAlaLeuAlaLysMetAlaThrAlaArgLysArgAlaGlnThrIleArgP 184
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     184 heSerTyrPheAlaLeuIleGlyMetArgAspGlyLysLeuCysLeuMet 200
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     551 TCAGCTACTTTGCACTTATAGGTATGAGAGATGGGAAGCTTTGCCTCATG 600

     201 TrpArgIleGlyAspPheArgProAsnHisValValGluGlyThrValAr 217
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     601 TGGCGCATTGGTGATTTTCGGCCAAACCACGTGGTAGAAGGAACAGTTAG 650

     217 gAlaGlnLeuLeuArgTyrThrGluAspSerGluGlyArgMetThrMetA 234
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     651 AGCCCAACTTCTCCGCTATACAGAAGACAGTGAAGGGAGGATGACGATGG 700

     234 laPheLysAspLeuLysLeuValAsnAspGlnIleIleLeuValThrPro 250
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     701 CATTTAAAGACCTCAAATTAGTCAACGACCAAATCATCCTGGTCACCCCG 750

     251 ValThrIleValHisGluIleAspHisGluSerProLeuTyrAlaLeuAs 267
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     751 GTAACTATTGTCCATGAAATTGACCATGAGAGCCCTCTGTATGCCCTTGA 800

     267 pArgLysAlaValAlaLysAspAsnPheGluIleLeuValThrPheIleT 284
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     801 CCGCAAAGCAGTAGCCAAAGATAACTTTGAGATTTTGGTGACATTTATCT 850

     284 yrThrGlyAspSerThrGlyThrSerHisGlnSerArgSerSerTyrVal 300
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     851 ATACTGGTGATTCCACTGGAACATCTCACCAATCTAGAAGCTCCTATGTT 900

     301 ProArg***IleLeuTrpGlyHisArgPheAsnAspValLeuGluValLy 317
         ||||||   ||||||||||||||||||||||||||||||||||||||||||
     901 CCCCGAGAAATTCTCTGGGGCCATAGGTTTAATGATGTCTTGGAAGTTAA 950

     317 sArgLysTyrTyrLysValAsnCysLeuGlnPheGluGlySerValGluV 334
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     951 GAGGAAGTATTACAAAGTGAACTGCTTACAGTTTGAAGGAAGTGTGGAAG 1000

     334 alTyrAlaProPheCysSerAlaLysGlnLeuAspTrpLysAspGlnGln 350
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    1001 TATATGCCCCCTTTTGCAGTGCCAAGCAATTGGACTGGAAAGACCAGCAG 1050

     351 LeuHisIleGluLysAlaProProValArgGluSerCysThrSerAspTh 367
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    1051 CTCCACATAGAAAAAGCACCACCAGTTCGAGAATCCTGCACGTCGGACAC 1100

     367 rLysAlaArgArgArgSerPheSerAlaValAlaIleValSerSer 382
         |||||||||||||||||||||||||||||||||||||||||||||
    1101 CAAGGCGAGACGAAGGTCATTTAGTGCAGTTGCCATTGTCAGCAGC 1146

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seq_documentation_block:
ID   AAS92631 standard; cDNA; 1395 BP.
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AC   AAS92631;
XX
DT   13-FEB-2002  (first entry)
XX
DE   DNA encoding novel human diagnostic protein #28435.
XX
KW   Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW   food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX
OS   Homo sapiens.
XX
PN   WO200175067-A2.
XX
PD   11-OCT-2001.
XX
PF   30-MAR-2001; 2001WO-US08631.
XX
PR   31-MAR-2000; 2000US-0540217.
PR   23-AUG-2000; 2000US-0649167.
XX
PA   (HYSE-) HYSEQ INC.
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```
XX
PI   Drmanac RT,  Liu C,  Tang YT;
XX
DR   WPI; 2001-639362/73.
DR   P-PSDB; ABG28444.
XX
PT   New isolated polynucleotide and encoded polypeptides, useful in
PT   diagnostics, forensics, gene mapping, identification of mutations
PT   responsible for genetic disorders or other traits and to assess
PT   biodiversity  -
XX
PS   Claim 1; SEQ ID No 28435; 103pp; English.
XX
CC   The invention relates to isolated polynucleotide (I) and
CC   polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC   polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC   and gene mapping, and in recombinant production of (II). The
CC   polynucleotides are also used in diagnostics as expressed sequence tags
CC   for identifying expressed genes. (I) is useful in gene therapy techniques
CC   to restore normal activity of (II) or to treat disease states involving
CC   (II). (II) is useful for generating antibodies against it, detecting or
CC   quantitating a polypeptide in tissue, as molecular weight markers and as
CC   a food supplement. (II) and its binding partners are useful in medical
CC   imaging of sites expressing (II). (I) and (II) are useful for treating
CC   disorders involving aberrant protein expression or biological activity.
CC   The polypeptide and polynucleotide sequences have applications in
CC   diagnostics, forensics, gene mapping, identification of mutations
CC   responsible for genetic disorders or other traits to assess biodiversity
CC   and to produce other types of data and products dependent on DNA and
CC   amino acid sequences. AAS64197-AAS94564 represent novel human
CC   diagnostic coding sequences of the invention.
CC   Note: The sequence data for this patent did not appear in the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 1395 BP; 410 A; 319 C; 299 G; 367 T; 0 other;


alignment_scores:
            Quality: 2011.00             Length:    382
              Ratio:  5.278               Gaps:      0
 Percent Similarity:  99.738   Percent Identity: 99.738

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      17 rProGlyTyrProProGluHisIleIleAlaGluLysArgArgAlaArgA 34
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     189 CCCAGGCTACCCGCCAGAGCACATTATAGCTGAGAAGAGAAGAGCAAGAA 238

      34 rgArgLeuLeuHisLysAspGlySerCysAsnValTyrPheLysHisIle 50
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     239 GACGATTACTTCACAAAGATGGCAGCTGTAATGTCTACTTCAAGCACATT 288

      51 PheGlyGluTrpGlySerTyrValValAspIlePheThrThrLeuValAs 67
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     289 TTTGGAGAATGGGGAAGCTATGTGGTTGACATCTTCACCACTCTTGTGGA 338

      67 pThrLysTrpArgHisMetPheValIlePheSerLeuSerTyrIleLeuS 84
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     339 CACCAAGTGGCGCCATATGTTTGTGATATTTTCTTTATCTTATATTCTCT 388

      84 erTrpLeuIlePheGlySerValPheTrpLeuIleAlaPheHisHisGly 100
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     389 CGTGGTTGATATTTGGCTCTGTCTTTTGGCTCATAGCCTTTCATCATGGC 438

     101 AspLeuLeuAsnAspProAspIleThrProCysValAspAsnValHisSe 117
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     439 GATCTATTAAATGATCCAGACATCACACCTTGTGTTGACAACGTCCATTC 488

     117 rPheThrGlyAlaPheLeuPheSerLeuGluThrGlnThrThrIleGlyT 134
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     489 TTTCACAGGGGCCTTTTTGTTCTCCCTAGAGACCCAAACCACCATAGGAT 538

     134 yrGlyTyrArgCysValThrGluGluCysSerValAlaValLeuMetVal 150
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     539 ATGGTTATCGCTGTGTTACTGAAGAATGTTCTGTGGCCGTGCTCATGGTG 588

     151 IleLeuGlnSerIleLeuSerCysIleIleAsnThrPheIleIleGlyAl 167
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     217 gAlaGlnLeuLeuArgTyrThrGluAspSerGluGlyArgMetThrMetA 234
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     267 pArgLysAlaValAlaLysAspAsnPheGluIleLeuValThrPheIleT 284
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    1039 CCCCGAGAAATTCTCTGGGGCCATAGGTTTAATGATGTCTTGGAAGTTAA 1088

     317 sArgLysTyrTyrLysValAsnCysLeuGlnPheGluGlySerValGluV 334
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    1089 GAGGAAGTATTACAAAGTGAACTGCTTACAGTTTGAAGGAAGTGTGGAAG 1138

     334 alTyrAlaProPheCysSerAlaLysGlnLeuAspTrpLysAspGlnGln 350
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    1139 TATATGCCCCCTTTTGCAGTGCCAAGCAATTGGACTGGAAAGACCAGCAG 1188

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seq_documentation_block:
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AC   AAD09566;
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DT   10-SEP-2001  (first entry)
XX
DE   Human transporter and ion channel-15 (TRICH-15) cDNA.
XX
KW   Human; transporter and ion channel-15; TRICH-15; cystic fibrosis; mood;
KW   gene therapy; amyotrophic lateral sclerosis; amnesia; muscular dystrophy;
KW   hypertension; angina; neurological disorder; asthma; bipolar disorder;
KW   dementia; depression; Alzheimer's disease; epilepsy; vaccine; arrhythmia;
KW   Pick's disease; ischaemic cerebrovascular disease; AIDS; anxiety; stroke;
KW   Huntington's disease; Parkinson's disease; cerebral neoplasm; allergy;
KW   demyelinating disease; mental disorder; Schizophrenia; polymyositis;
KW   muscle disorder; cardiomyopathy; cataract; myocarditis; Grave's disease;
KW   dermatomyositis; diabetes mellitus; immunological disorder; psoriasis;
KW   rheumatoid arthritis; Sjogren's syndrome; systemic lupus erythematosus;
KW   sickle cell anaemia; Wilson's disease; infertility; Cushing's disease;
KW   scleroderma; pulmonary artery stenosis; nootropic; Addison's disease;
KW   malabsorption syndrome; hypercholesterolaemia; cancer; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
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FT   sig_peptide     22..117
FT                   /*tag=  b
FT   mat_peptide     118..1380
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FT                   /product= "Mature human TRICH-15 protein"
XX
PN   WO200146258-A2.
XX
PD   28-JUN-2001.
XX
PF   22-DEC-2000; 2000WO-US35095.
XX
PR   23-DEC-1999;   99US-0172000.
PR   14-JAN-2000; 2000US-0176083.
PR   21-JAN-2000; 2000US-0177332.
PR   28-JAN-2000; 2000US-0178572.
PR   02-FEB-2000; 2000US-0179758.
PR   10-FEB-2000; 2000US-0181625.
XX
PA   (INCY-) INCYTE GENOMICS INC.
XX
PI   Baughn MR,  Burford N,  Au-Young J,  Lu DAM,  Yang J,  Reddy R,  Lal P;
PI   Hillman JL,  Azimzai Y,  Yue H,  Nguyen DB,  Yao MG,  Gandhi AR;
PI   Tang YT,  Khan FA;
XX
DR   WPI; 2001-418042/44.
DR   P-PSDB; AAE04902.
XX
PT   Novel human transporter and ion channel proteins useful for treating
PT   and preventing transport, neurological, muscle and immunological
PT   disorders  -
XX
PS   Claim 5; Page 150-151; 160pp; English.
XX
CC   The present sequence is transporter and ion channel-15 (TRICH-15) cDNA.
CC   TRICH is used as vaccine. TRICH is useful for treating a disease or
CC   condition associated with decreased expression of functional TRICH,
CC   such as transport disorder including amyotrophic lateral sclerosis,
CC   cystic fibrosis, Becker's muscular dystrophy, Charcot-Marie Tooth
CC   disease, Duchenne muscular dystrophy, angina and hypertension,
CC   neurological disorders including Alzheimer's disease, amnesia, bipolar
CC   disorder, dementia, depression, epilepsy, ischaemic cerebrovascular
CC   disease, stroke, cerebral neoplasms, Pick's disease, Huntington's
CC   disease and Parkinson's disease, demyelinating diseases, mental disorders
CC   including mood, anxiety, Schizophrenia and seasonal affective disorder,
CC   muscle disorder including cardiomyopathy, myocarditis, polymyositis,
CC   dermatomyositis, arrhythmias and asthma and immunological disorders
CC   including AIDS, adult respiratory distress syndrome (ARDS), allergies,
CC   anaemia, diabetes mellitus, rheumatoid arthritis, scleroderma, Sjogren's
CC   syndrome, systemic lupus erythematosus and other diseases including
CC   sickle cell anaemia, Wilson's disease, cataracts, infertility, pulmonary
CC   artery stenosis, Grave's disease, Cushing's disease, Addison's disease,
CC   glucose-galactose malabsorption syndrome, hypercholesterolaemia, cancers
CC   psoriasis and viral, bacterial, fungal, helminthic and protozoal
CC   infections. TRICH DNA is useful in gene therapy and in diagnostic
CC   purposes.
XX
SQ   Sequence 1730 BP; 520 A; 358 C; 361 G; 491 T; 0 other;


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            Quality: 2011.00              Length:    382
              Ratio:  5.278                 Gaps:      0
 Percent Similarity:  99.738   Percent Identity: 99.738

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      17 rProGlyTyrProProGluHisIleIleAlaGluLysArgArgAlaArgA 34
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     177 CCCAGGCTACCCGCCAGAGCACATTATAGCTGAGAAGAGAAGAGCAAGAA 226

      34 rgArgLeuLeuHisLysAspGlySerCysAsnValTyrPheLysHisIle 50
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     227 GACGATTACTTCACAAAGATGGCAGCTGTAATGTCTACTTCAAGCACATT 276

      51 PheGlyGluTrpGlySerTyrValValAspIlePheThrThrLeuValAs 67
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     277 TTTGGAGAATGGGGAAGCTATGTGGTTGACATCTTCACCACTCTTGTGGA 326

      67 pThrLysTrpArgHisMetPheValIlePheSerLeuSerTyrIleLeuS 84
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     327 CACCAAGTGGCGCCATATGTTTGTGATATTTTCTTTATCTTATATTCTCT 376

      84 erTrpLeuIlePheGlySerValPheTrpLeuIleAlaPheHisHisGly 100
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     377 CGTGGTTGATATTTGGCTCTGTCTTTTGGCTCATAGCCTTTCATCATGGC 426

     101 AspLeuLeuAsnAspProAspIleThrProCysValAspAsnValHisSe 117
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     427 GATCTATTAAATGATCCAGACATCACACCTTGTGTTGACAACGTCCATTC 476

     117 rPheThrGlyAlaPheLeuPheSerLeuGluThrGlnThrThrIleGlyT 134
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     477 TTTCACAGGGGCCTTTTTGTTCTCCCTAGAGACCCAAACCACCATAGGAT 526

     134 yrGlyTyrArgCysValThrGluGluCysSerValAlaValLeuMetVal 150
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     527 ATGGTTATCGCTGTGTTACTGAAGAATGTTCTGTGGCCGTGCTCATGGTG 576

     151 IleLeuGlnSerIleLeuSerCysIleIleAsnThrPheIleIleGlyAl 167
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     577 ATCCTCCAGTCCATCTTAAGTTGCATCATAAATACCTTTATCATTGGAGC 626

     167 aAlaLeuAlaLysMetAlaThrAlaArgLysArgAlaGlnThrIleArgP 184
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     627 TGCCTTGGCCAAAATGGCAACTGCTCGAAAGAGAGCCCAAACCATTCGTT 676

     184 heSerTyrPheAlaLeuIleGlyMetArgAspGlyLysLeuCysLeuMet 200
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     677 TCAGCTACTTTGCACTTATAGGTATGAGAGATGGGAAGCTTTGCCTCATG 726

     201 TrpArgIleGlyAspPheArgProAsnHisValValGluGlyThrValAr 217
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     727 TGGCGCATTGGTGATTTTCGGCCAAACCACGTGGTAGAAGGAACAGTTAG 776
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     217 gAlaGlnLeuLeuArgTyrThrGluAspSerGluGlyArgMetThrMetA 234
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     777 AGCCCAACTTCTCCGCTATACAGAAGACAGTGAAGGGAGGATGACGATGG 826

     234 laPheLysAspLeuLysLeuValAsnAspGlnIleIleLeuValThrPro 250
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     827 CATTTAAAGACCTCAAATTAGTCAACGACCAAATCATCCTGGTCACCCCG 876

     251 ValThrIleValHisGluIleAspHisGluSerProLeuTyrAlaLeuAs 267
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     877 GTAACTATTGTCCATGAAATTGACCATGAGAGCCCTCTGTATGCCCTTGA 926

     267 pArgLysAlaValAlaLysAspAsnPheGluIleLeuValThrPheIleT 284
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     927 CCGCAAAGCAGTAGCCAAAGATAACTTTGAGATTTTGGTGACATTTATCT 976

     284 yrThrGlyAspSerThrGlyThrSerHisGlnSerArgSerSerTyrVal 300
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     977 ATACTGGTGATTCCACTGGAACATCTCACCAATCTAGAAGCTCCTATGTT 1026

     301 ProArg***IleLeuTrpGlyHisArgPheAsnAspValLeuGluValLy 317
         ||||||   ||||||||||||||||||||||||||||||||||||||||||
    1027 CCCCGAGAAATTCTCTGGGGCCATAGGTTTAATGATGTCTTGGAAGTTAA 1076

     317 sArgLysTyrTyrLysValAsnCysLeuGlnPheGluGlySerValGluV 334
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    1077 GAGGAAGTATTACAAAGTGAACTGCTTACAGTTTGAAGGAAGTGTGGAAG 1126

     334 alTyrAlaProPheCysSerAlaLysGlnLeuAspTrpLysAspGlnGln 350
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    1127 TATATGCCCCCTTTTGCAGTGCCAAGCAATTGGACTGGAAAGACCAGCAG 1176

     351 LeuHisIleGluLysAlaProProValArgGluSerCysThrSerAspTh 367
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    1177 CTCCACATAGAAAAAGCACCACCAGTTCGAGAATCCTGCACGTCGGACAC 1226

     367 rLysAlaArgArgArgSerPheSerAlaValAlaIleValSerSer 382
         |||||||||||||||||||||||||||||||||||||||||||||
    1227 CAAGGCGAGACGAAGGTCATTTAGTGCAGTTGCCATTGTCAGCAGC 1272
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seq_name: /SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA2001A.DAT:AAK05088

seq_documentation_block:

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ID   AAK05088 standard; DNA; 1921 BP.
XX
AC   AAK05088;
XX
DT   05-NOV-2001  (first entry)
XX
DE   Human brain expressed single exon probe SEQ ID NO: 5079.
XX
KW   Human; brain expressed exon; gene expression analysis; probe;
KW   microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;
KW   epilepsy; cancer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200157275-A2.
XX
PD   09-AUG-2001.
XX
PF   30-JAN-2001; 2001WO-US00667.
XX
PR   04-FEB-2000; 2000US-0180312.
PR   26-MAY-2000; 2000US-0207456.
PR   30-JUN-2000; 2000US-0608408.
PR   03-AUG-2000; 2000US-0632366.
PR   21-SEP-2000; 2000US-0234687.
PR   27-SEP-2000; 2000US-0236359.
PR   04-OCT-2000; 2000GB-0024263.
XX
PA   (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI   Penn SG,  Hanzel DK,  Chen W,  Rank DR;
XX
DR   WPI; 2001-483446/52.
XX
PT   Single exon nucleic acid probes for analyzing gene expression in human
PT   brains -
XX
PS   Example 4; SEQ ID NO: 5079; 650pp + Sequence Listing; English.
XX
CC   The present invention provides a number of single exon nucleic acid
CC   probes which are derived from genomic sequences expressed in the human
CC   brain. They can be used to measure gene expression in brain cell samples,
CC   which may enable the diagnosis and improved treatment of nervous system
CC   diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
CC   epilepsy and cancers. The present sequence is one of the probes of the
CC   invention.
XX
SQ   Sequence 1921 BP; 573 A; 386 C; 395 G; 567 T; 0 other;
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alignment_scores:

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            Quality: 2011.00              Length:    382
              Ratio:  5.278                Gaps:      0
 Percent Similarity:  99.738   Percent Identity: 99.738
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alignment_block:

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 Align seg 1/1  to: AAK05088  from: 1  to: 1921

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         ||||||||||||||||||||||||||||||||||||||||||||||||||
     335 ATGAGCTATTACGGCAGCAGCTATCATATTATCAATGCGGACGCAAAATA 384

      17 rProGlyTyrProProGluHisIleIleAlaGluLysArgArgAlaArgA 34
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     385 CCCAGGCTACCCGCCAGAGCACATTATAGCTGAGAAGAGAAGAGCAAGAA 434

      34 rgArgLeuLeuHisLysAspGlySerCysAsnValTyrPheLysHisIle 50
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     435 GACGATTACTTCACAAAGATGGCAGCTGTAATGTCTACTTCAAGCACATT 484

      51 PheGlyGluTrpGlySerTyrValValAspIlePheThrThrLeuValAs 67
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     485 TTTGGAGAATGGGGAAGCTATGTGGTTGACATCTTCACCACTCTTGTGGA 534

      67 pThrLysTrpArgHisMetPheValIlePheSerLeuSerTyrIleLeuS 84
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     535 CACCAAGTGGCGCCATATGTTTGTGATATTTTCTTTATCTTATATTCTCT 584

      84 erTrpLeuIlePheGlySerValPheTrpLeuIleAlaPheHisHisGly 100
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     585 CGTGGTTGATATTTGGCTCTGTCTTTTGGCTCATAGCCTTTCATCATGGC 634

     101 AspLeuLeuAsnAspProAspIleThrProCysValAspAsnValHisSe 117
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     635 GATCTATTAAATGATCCAGACATCACACCTTGTGTTGACAACGTCCATTC 684

     117 rPheThrGlyAlaPheLeuPheSerLeuGluThrGlnThrThrIleGlyT 134
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     685 TTTCACAGGGGCCTTTTTGTTCTCCCTAGAGACCCAAACCACCATAGGAT 734

     134 yrGlyTyrArgCysValThrGluGluCysSerValAlaValLeuMetVal 150
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     735 ATGGTTATCGCTGTGTTACTGAAGAATGTTCTGTGGCCGTGCTCATGGTG 784

     151 IleLeuGlnSerIleLeuSerCysIleIleAsnThrPheIleIleGlyAl 167
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     785 ATCCTCCAGTCCATCTTAAGTTGCATCATAAATACCTTTATCATTGGAGC 834

     167 aAlaLeuAlaLysMetAlaThrAlaArgLysArgAlaGlnThrIleArgP 184
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     885 TCAGCTACTTTGCACTTATAGGTATGAGAGATGGGAAGCTTTGCCTCATG 934

     201 TrpArgIleGlyAspPheArgProAsnHisValValGluGlyThrValAr 217
         |||||||||||||||||||||||||||||||||||||||||||||||||||
     935 TGGCGCATTGGTGATTTTCGGCCAAACCACGTGGTAGAAGGAACAGTTAG 984

     217 gAlaGlnLeuLeuArgTyrThrGluAspSerGluGlyArgMetThrMetA 234
         |||||||||||||||||||||||||||||||||||||||||||||||||||
     985 AGCCCAACTTCTCCGCTATACAGAAGACAGTGAAGGGAGGATGACGATGG 1034

     234 laPheLysAspLeuLysLeuValAsnAspGlnIleIleLeuValThrPro 250
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    1035 CATTTAAAGACCTCAAATTAGTCAACGACCAAATCATCCTGGTCACCCCG 1084

     251 ValThrIleValHisGluIleAspHisGluSerProLeuTyrAlaLeuAs 267
         |||||||||||||||||||||||||||||||||||||||||||||||||||
    1085 GTAACTATTGTCCATGAAATTGACCATGAGAGCCCTCTGTATGCCCTTGA 1134

     267 pArgLysAlaValAlaLysAspAsnPheGluIleLeuValThrPheIleT 284
         |||||||||||||||||||||||||||||||||||||||||||||||||||
    1135 CCGCAAAGCAGTAGCCAAAGATAACTTTGAGATTTTGGTGACATTTATCT 1184

     284 yrThrGlyAspSerThrGlyThrSerHisGlnSerArgSerSerTyrVal 300
         |||||||||||||||||||||||||||||||||||||||||||||||||||
    1185 ATACTGGTGATTCCACTGGAACATCTCACCAATCTAGAAGCTCCTATGTT 1234

     301 ProArg***IleLeuTrpGlyHisArgPheAsnAspValLeuGluValLy 317
         ||||||   |||||||||||||||||||||||||||||||||||||||||||
    1235 CCCCGAGAAATTCTCTGGGGCCATAGGTTTAATGATGTCTTGGAAGTTAA 1284

     317 sArgLysTyrTyrLysValAsnCysLeuGlnPheGluGlySerValGluV 334
         |||||||||||||||||||||||||||||||||||||||||||||||||||
    1285 GAGGAAGTATTACAAAGTGAACTGCTTACAGTTTGAAGGAAGTGTGGAAG 1334

     334 alTyrAlaProPheCysSerAlaLysGlnLeuAspTrpLysAspGlnGln 350
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    1335 TATATGCCCCCTTTTGCAGTGCCAAGCAATTGGACTGGAAAGACCAGCAG 1384

     351 LeuHisIleGluLysAlaProProValArgGluSerCysThrSerAspTh 367
         |||||||||||||||||||||||||||||||||||||||||||||||||||
    1385 CTCCACATAGAAAAAGCACCACCAGTTCGAGAATCCTGCACGTCGGACAC 1434

     367 rLysAlaArgArgArgSerPheSerAlaValAlaIleValSerSer 382
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    1435 CAAGGCGAGACGAAGGTCATTTAGTGCAGTTGCCATTGTCAGCAGC 1480

seq_name: /SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA2001A.DAT:AAI36580

seq_documentation_block:
ID   AAI36580 standard; DNA; 1921 BP.
XX
AC   AAI36580;
XX
DT   17-OCT-2001  (first entry)
XX
DE   Probe #5266 used to measure gene expression in human placenta sample.
XX
KW   Probe; microarray; human; placenta; antenatal diagnosis;
KW   genetic disorder; ss.
XX
OS   Homo sapiens.
XX
PN   WO200157272-A2.
XX
PD   09-AUG-2001.
XX
PF   30-JAN-2001; 2001WO-US00663.
XX
PR   04-FEB-2000; 2000US-0180312.
PR   26-MAY-2000; 2000US-0207456.
PR   30-JUN-2000; 2000US-0608408.
PR   03-AUG-2000; 2000US-0632366.
PR   21-SEP-2000; 2000US-0234687.
PR   27-SEP-2000; 2000US-0236359.
PR   04-OCT-2000; 2000GB-0024263.
XX
PA   (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI   Penn SG,  Hanzel DK,  Chen W,  Rank DR;
XX
DR   WPI; 2001-488897/53.
XX
PT   Human genome-derived single exon nucleic acid probes useful for
PT   analyzing gene expression in human placenta -
XX
PS   Claim 25; SEQ ID No 5266; 654pp; English.
XX
CC   The present invention relates to single exon nucleic acid probes (SENP).
CC   The present sequence is one such probe. The probes are useful for
CC   producing a microarray for predicting, measuring and displaying gene
CC   expression in samples derived from human placenta. The probes are useful
CC   for antenatal diagnosis of human genetic disorders.
XX
SQ   Sequence 1921 BP; 573 A; 386 C; 395 G; 567 T; 0 other;


alignment_scores:
            Quality: 2011.00              Length:    382
              Ratio:  5.278                Gaps:      0
 Percent Similarity:  99.738   Percent Identity: 99.738

alignment_block:
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     335 ATGAGCTATTACGGCAGCAGCTATCATATTATCAATGCGGACGCAAAATA 384

      17 rProGlyTyrProProGluHisIleIleAlaGluLysArgArgAlaArgA 34
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     385 CCCAGGCTACCCGCCAGAGCACATTATAGCTGAGAAGAGAAGAGCAAGAA 434

      34 rgArgLeuLeuHisLysAspGlySerCysAsnValTyrPheLysHisIle 50
         |||||||||||||||||||||||||||||||||||||||||||||||||||
     435 GACGATTACTTCACAAAGATGGCAGCTGTAATGTCTACTTCAAGCACATT 484

      51 PheGlyGluTrpGlySerTyrValValAspIlePheThrThrLeuValAs 67
         |||||||||||||||||||||||||||||||||||||||||||||||||||
     485 TTTGGAGAATGGGGAAGCTATGTGGTTGACATCTTCACCACTCTTGTGGA 534

      67 pThrLysTrpArgHisMetPheValIlePheSerLeuSerTyrIleLeuS 84
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      84 erTrpLeuIlePheGlySerValPheTrpLeuIleAlaPheHisHisGly 100
         |||||||||||||||||||||||||||||||||||||||||||||||||||
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         |||||||||||||||||||||||||||||||||||||||||||||||||||
     635 GATCTATTAAATGATCCAGACATCACACCTTGTGTTGACAACGTCCATTC 684

     117 rPheThrGlyAlaPheLeuPheSerLeuGluThrGlnThrThrIleGlyT 134
         |||||||||||||||||||||||||||||||||||||||||||||||||||
     685 TTTCACAGGGGCCTTTTTGTTCTCCCTAGAGACCCAAACCACCATAGGAT 734

     134 yrGlyTyrArgCysValThrGluGluCysSerValAlaValLeuMetVal 150
         |||||||||||||||||||||||||||||||||||||||||||||||||||
     735 ATGGTTATCGCTGTGTTACTGAAGAATGTTCTGTGGCCGTGCTCATGGTG 784
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     151 IleLeuGlnSerIleLeuSerCysIleIleAsnThrPheIleIleGlyAl 167
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     167 aAlaLeuAlaLysMetAlaThrAlaArgLysArgAlaGlnThrIleArgP 184
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     184 heSerTyrPheAlaLeuIleGlyMetArgAspGlyLysLeuCysLeuMet 200
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     201 TrpArgIleGlyAspPheArgProAsnHisValValGluGlyThrValAr 217
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     935 TGGCGCATTGGTGATTTTCGGCCAAACCACGTGGTAGAAGGAACAGTTAG 984

     217 gAlaGlnLeuLeuArgTyrThrGluAspSerGluGlyArgMetThrMetA 234
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    1035 CATTTAAAGACCTCAAATTAGTCAACGACCAAATCATCCTGGTCACCCCG 1084

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         ||||||||||||||||||||||||||||||||||||||||||||||||||
    1085 GTAACTATTGTCCATGAAATTGACCATGAGAGCCCTCTGTATGCCCTTGA 1134

     267 pArgLysAlaValAlaLysAspAsnPheGluIleLeuValThrPheIleT 284
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     317 sArgLysTyrTyrLysValAsnCysLeuGlnPheGluGlySerValGluV 334
         ||||||||||||||||||||||||||||||||||||||||||||||||||
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seq_name: /SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA2001A.DAT:AAF85050

seq_documentation_block:
ID   AAF85050 standard; cDNA; 1257 BP.
XX
AC   AAF85050;
XX
DT   09-JUL-2001  (first entry)
XX
DE   Nucleotide sequence of a rat Kir5.1 polypeptide.
XX
KW   Kir5.1; inwardly rectifying potassium channel; ion channel;
KW   renal failure; hypokalemia; hypertension; hypotension; thyroid disease;
KW   pancreatitis; ss.
XX
OS   Rattus sp.
XX
FH   Key             Location/Qualifiers
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FT                   /*tag= a
FT                   /product= "Kir5.1"
FT                   /note= "no termination codon given"
XX
PN   WO200125258-A1.
XX
PD   12-APR-2001.
XX
PF   29-SEP-2000; 2000WO-US26996.
XX
PR   04-OCT-1999;   99US-0157491.
XX
PA   (MERI ) MERCK & CO INC.
XX
PI   Swanson RJ,  Liu Y,  McKenna E;
XX
DR   WPI; 2001-290604/30.
DR   P-PSDB; AAB68277.
XX
PT   Novel nucleic acid encoding human Kir5.1 subunit protein useful for
PT   identifying activators and inhibitors of potassium channels containing
PT   the protein subunit useful for treating various diseases  -
XX
PS   Disclosure; Fig 4A-B; 52pp; English.
XX
CC   The present sequence encodes a rat Kir5.1 subunit protein. Kir5.1
CC   is an inwardly rectifying potassium channel subunit. Kir5.1 proteins
CC   are useful for identifying inhibitors or activators of potassium
CC   channels. Kir5.1 proteins are useful as attractive targets for drug
CC   discovery and as valuable research tools for understanding ion channel
CC   biology. Kir5.1 proteins are also useful for identifying inhibitors or
CC   activators of potassium channels. Inhibitors or activators screened
CC   using Kir5.1 protein are useful for treating a variety of diseases
CC   involving excessive or insufficient potassium channel activity, such as
CC   renal failure, hypokalemia, hypertension, hypotension, thyroid disease
CC   and pancreatitis.
XX
SQ   Sequence 1257 BP; 325 A; 325 C; 314 G; 293 T; 0 other;


alignment_scores:
            Quality: 1898.50              Length:    383
              Ratio:  5.036                Gaps:      1
 Percent Similarity:  98.433   Percent Identity: 93.473

alignment_block:
 US-09-623-304A-1 x AAF85050   ..

 Align seg 1/1  to: AAF85050  from: 1  to: 1257

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      17 rProGlyTyrProProGluHisIleIleAlaGluLysArgArgAlaArgA 34
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      34 rgArgLeuLeuHisLysAspGlySerCysAsnValTyrPheLysHisIle 50
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     101 GGCGCCTGCTCCACAAAGATGGCAGCTGTAACGTGTACTTTAAACACATT 150

      51 PheGlyGluTrpGlySerTyrValValAspIlePheThrThrLeuValAs 67
         ||||||||||||||||||:::|||||||||||||||||||||||||||||
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      67 pThrLysTrpArgHisMetPheValIlePheSerLeuSerTyrIleLeuS 84
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     201 TACCAAGTGGCGCCATATGTTTGTAGTATTTTCTTTGTCTTACATTCTCT 250

      84 erTrpLeuIlePheGlySerValPheTrpLeuIleAlaPheHisHisGly 100
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  101 AspLeuLeuAsnAspProAspIleThrProCysValAspAsnValHisSe 117
      |||||||||:::|||||||||||||||||||||||||||||||||||||
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  117 rPheThrGlyAlaPheLeuPheSerLeuGluThrGlnThrThrIleGlyT 134
      |||||||:::|||||||||||||||||||||||||||||||||||||||
  351 ATTTACGGCTGCGTTTTTATTCTCCCTTGAGACCCAAACCACCATCGGGT 400

  134 yrGlyTyrArgCysValThrGluGluCysSerValAlaValLeuMetVal 150
      |||||||||||||||||||||||||||||||||||||||||||   |||
  401 ACGGTTACCGTTGTGTCACGGAAGAATGCTCTGTGGCCGTGCTGACGGTC 450

  151 IleLeuGlnSerIleLeuSerCysIleIleAsnThrPheIleIleGlyAl 167
      |||||||||||||||||||||||||||||||||||||||||||||||||
  451 ATCCTTCAGTCCATCCTGAGCTGCATCATAAACACCTTCATCATTGGGGC 500

  167 aAlaLeuAlaLysMetAlaThrAlaArgLysArgAlaGlnThrIleArgP 184
      |||||||||||||||||||||||||||||||||||||||||||||||||
  501 AGCCTTGGCAAAGATGGCGACCGCCCGGAAGCGAGCCCAGACCATCCGCT 550

  184 heSerTyrPheAlaLeuIleGlyMetArgAspGlyLysLeuCysLeuMet 200
      |||||||||||||||||||||||||||||||||||||||||||||||||
  551 TCAGCTATTTCGCACTCATCGGCATGAGAGACGGGAAGCTTTGCCTCATG 600

  201 TrpArgIleGlyAspPheArgProAsnHisValValGluGlyThrValAr 217
      |||||||||||||||||||||||||||||||||||||||||||||||||
  601 TGGCGCATAGGTGACTTCCGACCGAACCATGTGGTGGAGGGCACGGTGAG 650

  217 gAlaGlnLeuLeuArgTyrThrGluAspSerGluGlyArgMetThrMetA 234
      |||||||||||||||||:::|||||||||||||||||||||||||||||
  651 AGCCCAACTTCTGCGCTATTCAGAAGACAGCGAAGGGCGGATGACGATGG 700

  234 laPheLysAspLeuLysLeuValAsnAspGlnIleIleLeuValThrPro 250
      |||||||||||||||||||||||||||||||||||||||||||||||||
  701 CGTTTAAAGACCTCAAACTCGTCAATGACCAGATAATCCTGGTAACGCCA 750

  251 ValThrIleValHisGluIleAspHisGluSerProLeuTyrAlaLeuAs 267
      |||||||||||||||||||||||||||||||||||||||||||||||||
  751 GTGACCATTGTCCATGAAATTGACCACGAGAGTCCTCTGTATGCCCTTGA 800

  267 pArgLysAlaValAlaLysAspAsnPheGluIleLeuValThrPheIleT 284
      |||||||||||||||||||||||||||||||||||||||||||||||||
  801 CCGCAAGGCAGTGGCCAAAGATAATTTCGAGATTCTGGTGACATTTATTT 850

  284 yrThrGlyAspSerThrGlyThrSerHisGlnSerArgSerSerTyrVal 300
      |||||||||||||||||||||||||||||||||||||||||||||||||
  851 ATACTGGTGACTCTACTGGGACATCCCACCAGTCCAGAAGTTCCTACGTC 900

  301 ProArg***IleLeuTrpGlyHisArgPheAsnAspValLeuGluValLy 317
      ||||||   |||||||||||||||||||:::|||||||||||||||||||
  901 CCCAGAGAAATTCTCTGGGGACACAGGTTTCATGATGTATTGGAAGTGAA 950

  317 sArgLysTyrTyrLysValAsnCysLeuGlnPheGluGlySerValGluV 334
      |||||||||||||||||||||||||||||||||||||||||||||||||
  951 GAGAAAGTACTACAAGGTAAACTGCTTGCAGTTTGAGGGAAGCGTGGAAG 1000

  334 alTyrAlaProPheCysSerAlaLysGlnLeuAspTrpLysAspGlnGln 350
      |||||||||||||||||||||||||||||||||||||||||||||||||
 1001 TCTACGCCCCCTTTTGCAGTGCCAAACAACTGGACTGGAAGGACCAACAG 1050

  351 Leu...HisIleGluLysAlaProProValArgGluSerCysThrSerAs 366
      |||   ::::::||||||:::   |||:::|||   |||||||||||||
 1051 CTCAACAACTTGGAGAAAACGTCCCCTGCCCGAGGATCCTGCACCTCGGA 1100

  366 pThrLysAlaArgArgArgSerPheSerAlaValAlaIleValSerSer 382
      ||||::::::|||||||||||||||||||||||||:::|||||||||
 1101 CACCAACACCAGGAGGAGATCCTTCAGCGCAGTTGCCATGGTGAGCAGC 1149
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seq_name: /SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA2001A.DAT:AAK17807

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XX
AC   AAK17807;
XX
DT   05-NOV-2001  (first entry)
XX
DE   Human brain expressed single exon probe SEQ ID NO: 17798.
XX
KW   Human; brain expressed exon; gene expression analysis; probe;
KW   microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;
KW   epilepsy; cancer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200157275-A2.
XX
PD   09-AUG-2001.
XX
PF   30-JAN-2001; 2001WO-US00667.
XX
PR   04-FEB-2000; 2000US-0180312.
PR   26-MAY-2000; 2000US-0207456.
PR   30-JUN-2000; 2000US-0608408.
PR   03-AUG-2000; 2000US-0632366.
PR   21-SEP-2000; 2000US-0234687.
PR   27-SEP-2000; 2000US-0236359.
PR   04-OCT-2000; 2000GB-0024263.
XX
PA   (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI   Penn SG,  Hanzel DK,  Chen W,  Rank DR;
XX
DR   WPI; 2001-483446/52.
XX
PT   Single exon nucleic acid probes for analyzing gene expression in human
PT   brains -
XX
PS   Example 4; SEQ ID NO: 17798; 650pp + Sequence Listing; English.
XX
CC   The present invention provides a number of single exon nucleic acid
CC   probes which are derived from genomic sequences expressed in the human
CC   brain. They can be used to measure gene expression in brain cell samples,
CC   which may enable the diagnosis and improved treatment of nervous system
CC   diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
CC   epilepsy and cancers. The present sequence is one of the probes of the
CC   invention.
XX
SQ   Sequence 1118 BP; 320 A; 250 C; 239 G; 309 T; 0 other;


alignment_scores:
           Quality: 1802.00              Length:    341
             Ratio:  5.300                Gaps:      0
 Percent Similarity:  99.707   Percent Identity: 99.707

alignment_block:
 US-09-623-304A-1 x AAK17807   ..

 Align seg 1/1  to: AAK17807  from: 1  to: 1118

       1 MetSerTyrTyrGlySerSerTyrHisIleIleAsnAlaAspAlaLysTy 17
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      94 ATGAGCTATTACGGCAGCAGCTATCATATTATCAATGCGGACGCAAAATA 143

      17 rProGlyTyrProProGluHisIleIleAlaGluLysArgArgAlaArgA 34
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     144 CCCAGGCTACCCGCCAGAGCACATTATAGCTGAGAAGAGAAGAGCAAGAA 193

      34 rgArgLeuLeuHisLysAspGlySerCysAsnValTyrPheLysHisIle 50
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     194 GACGATTACTTCACAAAGATGGCAGCTGTAATGTCTACTTCAAGCACATT 243
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 51 PheGlyGluTrpGlySerTyrValValAspIlePheThrThrLeuValAs 67
    ||||||||||||||||||||||||||||||||||||||||||||||||||
244 TTTGGAGAATGGGGAAGCTATGTGGTTGACATCTTCACCACTCTTGTGGA 293

 67 pThrLysTrpArgHisMetPheValIlePheSerLeuSerTyrIleLeuS 84
    ||||||||||||||||||||||||||||||||||||||||||||||||||
294 CACCAAGTGGCGCCATATGTTTGTGATATTTTCTTTATCTTATATTCTCT 343

 84 erTrpLeuIlePheGlySerValPheTrpLeuIleAlaPheHisHisGly 100
    ||||||||||||||||||||||||||||||||||||||||||||||||||
344 CGTGGTTGATATTTGGCTCTGTCTTTTGGCTCATAGCCTTTCATCATGGC 393

101 AspLeuLeuAsnAspProAspIleThrProCysValAspAsnValHisSe 117
    ||||||||||||||||||||||||||||||||||||||||||||||||||
394 GATCTATTAAATGATCCAGACATCACACCTTGTGTTGACAACGTCCATTC 443

117 rPheThrGlyAlaPheLeuPheSerLeuGluThrGlnThrThrIleGlyT 134
    ||||||||||||||||||||||||||||||||||||||||||||||||||
444 TTTCACAGGGGCCTTTTTGTTCTCCCTAGAGACCCAAACCACCATAGGAT 493

134 yrGlyTyrArgCysValThrGluGluCysSerValAlaValLeuMetVal 150
    ||||||||||||||||||||||||||||||||||||||||||||||||||
494 ATGGTTATCGCTGTGTTACTGAAGAATGTTCTGTGGCCGTGCTCATGGTG 543

151 IleLeuGlnSerIleLeuSerCysIleIleAsnThrPheIleIleGlyAl 167
    ||||||||||||||||||||||||||||||||||||||||||||||||||
544 ATCCTCCAGTCCATCTTAAGTTGCATCATAAATACCTTTATCATTGGAGC 593

167 aAlaLeuAlaLysMetAlaThrAlaArgLysArgAlaGlnThrIleArgP 184
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594 TGCCTTGGCCAAAATGGCAACTGCTCGAAAGAGAGCCCAAACCATTCGTT 643

184 heSerTyrPheAlaLeuIleGlyMetArgAspGlyLysLeuCysLeuMet 200
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644 TCAGCTACTTTGCACTTATAGGTATGAGAGATGGGAAGCTTTGCCTCATG 693

201 TrpArgIleGlyAspPheArgProAsnHisValValGluGlyThrValAr 217
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694 TGGCGCATTGGTGATTTTCGGCCAAACCACGTGGTAGAAGGAACAGTTAG 743

217 gAlaGlnLeuLeuArgTyrThrGluAspSerGluGlyArgMetThrMetA 234
    ||||||||||||||||||||||||||||||||||||||||||||||||||
744 AGCCCAACTTCTCCGCTATACAGAAGACAGTGAAGGGAGGATGACGATGG 793

234 laPheLysAspLeuLysLeuValAsnAspGlnIleIleLeuValThrPro 250
    ||||||||||||||||||||||||||||||||||||||||||||||||||
794 CATTTAAAGACCTCAAATTAGTCAACGACCAAATCATCCTGGTCACCCCG 843

251 ValThrIleValHisGluIleAspHisGluSerProLeuTyrAlaLeuAs 267
    ||||||||||||||||||||||||||||||||||||||||||||||||||
844 GTAACTATTGTCCATGAAATTGACCATGAGAGCCCTCTGTATGCCCTTGA 893

267 pArgLysAlaValAlaLysAspAsnPheGluIleLeuValThrPheIleT 284
    ||||||||||||||||||||||||||||||||||||||||||||||||||
894 CCGCAAAGCAGTAGCCAAAGATAACTTTGAGATTTTGGTGACATTTATCT 943

284 yrThrGlyAspSerThrGlyThrSerHisGlnSerArgSerSerTyrVal 300
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944 ATACTGGTGATTCCACTGGAACATCTCACCAATCTAGAAGCTCCTATGTT 993

301 ProArg***IleLeuTrpGlyHisArgPheAsnAspValLeuGluValLy 317
    ||||||   ||||||||||||||||||||||||||||||||||||||||||
994 CCCCGAGAAATTCTCTGGGGCCATAGGTTTAATGATGTCTTGGAAGTTAA 1043

317 sArgLysTyrTyrLysValAsnCysLeuGlnPheGluGlySerValGluV 334
    ||||||||||||||||||||||||||||||||||||||||||||||||||
1044 GAGGAAGTATTACAAAGTGAACTGCTTACAGTTTGAAGGAAGTGTGGAAG 1093

334 alTyrAlaProPheCysSerAla 341
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1094 TATATGCCCCCTTTTGCAGTGCC 1116
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XX
AC   AAI49699;
XX
DT   17-OCT-2001  (first entry)
XX
DE   Probe #18385 used to measure gene expression in human placenta sample.
XX
KW   Probe; microarray; human; placenta; antenatal diagnosis;
KW   genetic disorder; ss.
XX
OS   Homo sapiens.
XX
PN   WO200157272-A2.
XX
PD   09-AUG-2001.
XX
PF   30-JAN-2001; 2001WO-US00663.
XX
PR   04-FEB-2000; 2000US-0180312.
PR   26-MAY-2000; 2000US-0207456.
PR   30-JUN-2000; 2000US-0608408.
PR   03-AUG-2000; 2000US-0632366.
PR   21-SEP-2000; 2000US-0234687.
PR   27-SEP-2000; 2000US-0236359.
PR   04-OCT-2000; 2000GB-0024263.
XX
PA   (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI   Penn SG,  Hanzel DK,  Chen W,  Rank DR;
XX
DR   WPI; 2001-488897/53.
XX
PT   Human genome-derived single exon nucleic acid probes useful for
PT   analyzing gene expression in human placenta -
XX
PS   Claim 25; SEQ ID No 18385; 654pp; English.
XX
CC   The present invention relates to single exon nucleic acid probes (SENP).
CC   The present sequence is one such probe. The probes are useful for
CC   producing a microarray for predicting, measuring and displaying gene
CC   expression in samples derived from human placenta. The probes are useful
CC   for antenatal diagnosis of human genetic disorders.
XX
SQ   Sequence 1118 BP; 320 A; 250 C; 239 G; 309 T; 0 other;


alignment_scores:
            Quality: 1802.00              Length:    341
              Ratio:  5.300                Gaps:      0
 Percent Similarity:  99.707   Percent Identity: 99.707

alignment_block:
 US-09-623-304A-1 x AAI49699   ..

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      94 ATGAGCTATTACGGCAGCAGCTATCATATTATCAATGCGGACGCAAAATA 143

      17 rProGlyTyrProProGluHisIleIleAlaGluLysArgArgAlaArgA 34
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     144 CCCAGGCTACCCGCCAGAGCACATTATAGCTGAGAAGAGAAGAGCAAGAA 193

      34 rgArgLeuLeuHisLysAspGlySerCysAsnValTyrPheLysHisIle 50
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     194 GACGATTACTTCACAAAGATGGCAGCTGTAATGTCTACTTCAAGCACATT 243

      51 PheGlyGluTrpGlySerTyrValValAspIlePheThrThrLeuValAs 67
         ||||||||||||||||||||||||||||||||||||||||||||||||||
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  244 TTTGGAGAATGGGGAAGCTATGTGGTTGACATCTTCACCACTCTTGTGGA 293

   67 pThrLysTrpArgHisMetPheValIlePheSerLeuSerTyrIleLeuS 84
      ||||||||||||||||||||||||||||||||||||||||||||||||||
  294 CACCAAGTGGCGCCATATGTTTGTGATATTTTCTTTATCTTATATTCTCT 343

   84 erTrpLeuIlePheGlySerValPheTrpLeuIleAlaPheHisHisGly 100
      ||||||||||||||||||||||||||||||||||||||||||||||||||
  344 CGTGGTTGATATTTGGCTCTGTCTTTTGGCTCATAGCCTTTCATCATGGC 393

  101 AspLeuLeuAsnAspProAspIleThrProCysValAspAsnValHisSe 117
      ||||||||||||||||||||||||||||||||||||||||||||||||||
  394 GATCTATTAAATGATCCAGACATCACACCTTGTGTTGACAACGTCCATTC 443

  117 rPheThrGlyAlaPheLeuPheSerLeuGluThrGlnThrThrIleGlyT 134
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  444 TTTCACAGGGGCCTTTTTGTTCTCCCTAGAGACCCAAACCACCATAGGAT 493

  134 yrGlyTyrArgCysValThrGluGluCysSerValAlaValLeuMetVal 150
      ||||||||||||||||||||||||||||||||||||||||||||||||||
  494 ATGGTTATCGCTGTGTTACTGAAGAATGTTCTGTGGCCGTGCTCATGGTG 543

  151 IleLeuGlnSerIleLeuSerCysIleIleAsnThrPheIleIleGlyAl 167
      ||||||||||||||||||||||||||||||||||||||||||||||||||
  544 ATCCTCCAGTCCATCTTAAGTTGCATCATAAATACCTTTATCATTGGAGC 593

  167 aAlaLeuAlaLysMetAlaThrAlaArgLysArgAlaGlnThrIleArgP 184
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  217 gAlaGlnLeuLeuArgTyrThrGluAspSerGluGlyArgMetThrMetA 234
      ||||||||||||||||||||||||||||||||||||||||||||||||||
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  234 laPheLysAspLeuLysLeuValAsnAspGlnIleIleLeuValThrPro 250
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  794 CATTTAAAGACCTCAAATTAGTCAACGACCAAATCATCCTGGTCACCCCG 843

  251 ValThrIleValHisGluIleAspHisGluSerProLeuTyrAlaLeuAs 267
      ||||||||||||||||||||||||||||||||||||||||||||||||||
  844 GTAACTATTGTCCATGAAATTGACCATGAGAGCCCTCTGTATGCCCTTGA 893

  267 pArgLysAlaValAlaLysAspAsnPheGluIleLeuValThrPheIleT 284
      ||||||||||||||||||||||||||||||||||||||||||||||||||
  894 CCGCAAAGCAGTAGCCAAAGATAACTTTGAGATTTTGGTGACATTTATCT 943

  284 yrThrGlyAspSerThrGlyThrSerHisGlnSerArgSerSerTyrVal 300
      ||||||||||||||||||||||||||||||||||||||||||||||||||
  944 ATACTGGTGATTCCACTGGAACATCTCACCAATCTAGAAGCTCCTATGTT 993

  301 ProArg***IleLeuTrpGlyHisArgPheAsnAspValLeuGluValLy 317
      ||||||   ||||||||||||||||||||||||||||||||||||||||||
  994 CCCCGAGAAATTCTCTGGGGCCATAGGTTTAATGATGTCTTGGAAGTTAA 1043

  317 sArgLysTyrTyrLysValAsnCysLeuGlnPheGluGlySerValGluV 334
      ||||||||||||||||||||||||||||||||||||||||||||||||||
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  334 alTyrAlaProPheCysSerAla 341
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XX
AC   AAX35738;
XX
DT   09-JUL-1999  (first entry)
XX
DE   cDNA encoding a protein identified by the signal sequence trap method.
XX
KW   Signal sequence trap method; SST method; immunisation; inhibition;
KW   infection; allergy; cancer; regulation; tissue formation; tissue repair;
KW   activin activity; inhibin activity; chemokine activity;
KW   cytokine activity; blood coagulation regulation; agonist; antagonist;
KW   metabolic disorder; hormonal disorder; immune disorder;
KW   severe combined immunodeficiency; SCID; AIDS; thrombosis; cancer;
KW   wound; ss.
XX
OS   Homo sapiens.
XX
PN   WO9918126-A1.
XX
PD   15-APR-1999.
XX
PF   06-OCT-1998;   98WO-JP04514.
XX
PR   07-OCT-1997;   97JP-0274674.
XX
PA   (ONOY ) ONO PHARM CO LTD.
XX
PI   Fukushima D,  Shibayama S,  Tada H;
XX
DR   WPI; 1999-277254/23.
DR   P-PSDB; AAY02380.
XX
PT   Polypeptides identified by the signal sequence trap method from a
PT   human cDNA library
XX
PS   Claim 5; Page 212; 281pp; Japanese.
XX
CC   AAX35694-X35747 represent cDNA sequences that encode novel polypeptides
CC   (AAY02358-84) which are identified from a human placental cDNA library
CC   by the signal sequence trap (SST) method. The polypeptides have a
CC   broad range of physiological activity, including immunisation against
CC   and inhibition of infections, allergies and cancer; regulation of tissue
CC   formation and repair; activin/inhibin activity; chemokine/cytokine
CC   activity; blood coagulation regulation; and receptor/ligand agonist
CC   or antagonist activity. The polypeptides can be used for prevention
CC   and treatment of disorders including infections by bacteria, yeasts and
CC   viruses (including HIV) and protozoa; metabolic and hormonal disorders;
CC   immune disorders (including severe combined immunodeficiency (SCID)
CC   and AIDS; thrombosis; cancer; and traumatic or surgical wounds.
XX
SQ   Sequence 765 BP; 206 A; 175 C; 167 G; 217 T; 0 other;


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             Ratio:  5.287             Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
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      34 rgArgLeuLeuHisLysAspGlySerCysAsnValTyrPheLysHisIle 50
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  51 PheGlyGluTrpGlySerTyrValValAspIlePheThrThrLeuValAs 67
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 151 TTTGGAGAATGGGGAAGCTATGTGGTTGACATCTTCACCACTCTTGTGGA 200

  67 pThrLysTrpArgHisMetPheValIlePheSerLeuSerTyrIleLeuS 84
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 201 CACCAAGTGGCGCCATATGTTTGTGATATTTTCTTTATCTTATATTCTCT 250

  84 erTrpLeuIlePheGlySerValPheTrpLeuIleAlaPheHisHisGly 100
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 251 CGTGGTTGATATTTGGCTCTGTCTTTTGGCTCATAGCCTTTCATCATGGC 300

 101 AspLeuLeuAsnAspProAspIleThrProCysValAspAsnValHisSe 117
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 301 GATCTATTAAATGATCCAGACATCACACCTTGTGTTGACAACGTCCATTC 350

 117 rPheThrGlyAlaPheLeuPheSerLeuGluThrGlnThrThrIleGlyT 134
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 351 TTTCACAGGGGCCTTTTGTTCTCCCTAGAGACCCAAACCACCATAGGAT 400

 134 yrGlyTyrArgCysValThrGluGluCysSerValAlaValLeuMetVal 150
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 401 ATGGTTATCGCTGTGTTACTGAAGAATGTTCTGTGGCCGTGCTCATGGTG 450

 151 IleLeuGlnSerIleLeuSerCysIleIleAsnThrPheIleIleGlyAl 167
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 451 ATCCTCCAGTCCATCTTAAGTTGCATCATAAATACCTTTATCATTGGAGC 500

 167 aAlaLeuAlaLysMetAlaThrAlaArgLysArgAlaGlnThrIleArgP 184
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 501 TGCCTTGGCCAAAATGGCAACTGCTCGAAAGAGAGCCCAAACCATTCGTT 550

 184 heSerTyrPheAlaLeuIleGlyMetArgAspGlyLysLeuCysLeuMet 200
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 551 TCAGCTACTTTGCACTTATAGGTATGAGAGATGGGAAGCTTTGCCTCATG 600

 201 TrpArgIleGlyAspPheArgProAsnHisValValGluGlyThrValAr 217
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 601 TGGCGCATTGGTGATTTCGGCCAAACCACGTGGTAGAAGGAACAGTTAG 650

 217 gAlaGlnLeuLeuArgTyrThrGluAspSerGluGlyArgMetThrMetA 234
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 651 AGCCCAACTTCTCCGCTATACAGAAGACAGTGAAGGGAGGATGACGATGG 700

 234 laPheLysAspLeuLysLeuValAsnAspGlnIleIleLeuValThrPro 250
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 701 CATTTAAAGACCTCAAATTAGTCAACGACCAAATCATCCTGGTCACCCCG 750

 251 ValThrIleVal 254
     ||||||||||||
 751 GTAACTATTGTC 762
```

seq_name: /SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA1999.DAT:AAX35739

```
seq_documentation_block:
ID   AAX35739 standard; cDNA; 907 BP.
XX
AC   AAX35739;
XX
DT   09-JUL-1999  (first entry)
XX
DE   cDNA encoding a protein identified by the signal sequence trap method.
XX
KW   Signal sequence trap method; SST method; immunisation; inhibition;
KW   infection; allergy; cancer; regulation; tissue formation; tissue repair;
KW   activin activity; inhibin activity; chemokine activity;
KW   cytokine activity; blood coagulation regulation; agonist; antagonist;
KW   metabolic disorder; hormonal disorder; immune disorder;
KW   severe combined immunodeficiency; SCID; AIDS; thrombosis; cancer;
KW   wound; ss.
XX
OS   Homo sapiens.
XX
PN   WO9918126-A1.
XX
PD   15-APR-1999.
XX
PF   06-OCT-1998;   98WO-JP04514.
XX
PR   07-OCT-1997;   97JP-0274674.
XX
PA   (ONOY ) ONO PHARM CO LTD.
XX
PI   Fukushima D,  Shibayama S,  Tada H;
XX
DR   WPI; 1999-277254/23.
DR   P-PSDB; AAY02380.
XX
PT   Polypeptides identified by the signal sequence trap method from a
PT   human cDNA library
XX
PS   Claim 4; Page 213-215; 281pp; Japanese.
XX
CC   AAX35694-X35747 represent cDNA sequences that encode novel polypeptides
CC   (AAY02358-84) which are identified from a human placental cDNA library
CC   by the signal sequence trap (SST) method. The polypeptides have a
CC   broad range of physiological activity, including immunisation against
CC   and inhibition of infections, allergies and cancer; regulation of tissue
CC   formation and repair; activin/inhibin activity; chemokine/cytokine
CC   activity; blood coagulation regulation; and receptor/ligand agonist
CC   or antagonist activity. The polypeptides can be used for prevention
CC   and treatment of disorders including infections by bacteria, yeasts and
CC   viruses (including HIV) and protozoa; metabolic and hormonal disorders;
CC   immune disorders (including severe combined immunodeficiency (SCID)
CC   and AIDS; thrombosis; cancer; and traumatic or surgical wounds.
XX
SQ   Sequence 907 BP; 278 A; 210 C; 183 G; 236 T; 0 other;


alignment_scores:
           Quality: 1343.00              Length:    254
             Ratio:  5.287                Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-623-304A-1 x AAX35739   ..

 Align seg 1/1  to: AAX35739  from: 1  to: 907

       1 MetSerTyrTyrGlySerSerTyrHisIleIleAsnAlaAspAlaLysTy 17
         ||||||||||||||||||||||||||||||||||||||||||||||||||
      78 ATGAGCTATTACGGCAGCAGCTATCATATTATCAATGCGGACGCAAAATA 127

      17 rProGlyTyrProProGluHisIleIleAlaGluLysArgArgAlaArgA 34
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     128 CCCAGGCTACCCGCCAGAGCACATTATAGCTGAGAAGAGAAGAGCAAGAA 177

      34 rgArgLeuLeuHisLysAspGlySerCysAsnValTyrPheLysHisIle 50
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     178 GACGATTACTTCACAAAGATGGCAGCTGTAATGTCTACTTCAAGCACATT 227

      51 PheGlyGluTrpGlySerTyrValValAspIlePheThrThrLeuValAs 67
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     228 TTTGGAGAATGGGGAAGCTATGTGGTTGACATCTTCACCACTCTTGTGGA 277

      67 pThrLysTrpArgHisMetPheValIlePheSerLeuSerTyrIleLeuS 84
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     278 CACCAAGTGGCGCCATATGTTTGTGATATTTTCTTTATCTTATATTCTCT 327

      84 erTrpLeuIlePheGlySerValPheTrpLeuIleAlaPheHisHisGly 100
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     328 CGTGGTTGATATTTGGCTCTGTCTTTTGGCTCATAGCCTTTCATCATGGC 377
```

```
     101 AspLeuLeuAsnAspProAspIleThrProCysValAspAsnValHisSe 117
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     378 GATCTATTAAATGATCCAGACATCACACCTTGTGTTGACAACGTCCATTC 427

     117 rPheThrGlyAlaPheLeuPheSerLeuGluThrGlnThrThrIleGlyT 134
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     428 TTTCACAGGGGCCTTTTTGTTCTCCCTAGAGACCCAAACCACCATAGGAT 477

     134 yrGlyTyrArgCysValThrGluGluCysSerValAlaValLeuMetVal 150
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     478 ATGGTTATCGCTGTGTTACTGAAGAATGTTCTGTGGCCGTGCTCATGGTG 527

     151 IleLeuGlnSerIleLeuSerCysIleIleAsnThrPheIleIleGlyAl 167
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     528 ATCCTCCAGTCCATCTTAAGTTGCATCATAAATACCTTTATCATTGGAGC 577

     167 aAlaLeuAlaLysMetAlaThrAlaArgLysArgAlaGlnThrIleArgP 184
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     578 TGCCTTGGCCAAAATGGCAACTGCTCGAAAGAGAGCCCAAACCATTCGTT 627

     184 heSerTyrPheAlaLeuIleGlyMetArgAspGlyLysLeuCysLeuMet 200
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     628 TCAGCTACTTTGCACTTATAGGTATGAGAGATGGGAAGCTTTGCCTCATG 677

     201 TrpArgIleGlyAspPheArgProAsnHisValValGluGlyThrValAr 217
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     678 TGGCGCATTGGTGATTTTCGGCCAAACCACGTGGTAGAAGGAACAGTTAG 727

     217 gAlaGlnLeuLeuArgTyrThrGluAspSerGluGlyArgMetThrMetA 234
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     728 AGCCCAACTTCTCCGCTATACAGAAGACAGTGAAGGGAGGATGACGATGG 777

     234 laPheLysAspLeuLysLeuValAsnAspGlnIleIleLeuValThrPro 250
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     778 CATTTAAAGACCTCAAATTAGTCAACGACCAAATCATCCTGGTCACCCCG 827

     251 ValThrIleVal 254
         ||||||||||||
     828 GTAACTATTGTC 839

seq_name: /SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA2001A.DAT:AAH21453

seq_documentation_block:
ID   AAH21453 standard; DNA; 1284 BP.
XX
AC   AAH21453;
XX
DT   18-SEP-2001  (first entry)
XX
DE   Human IRK1 DNA.
XX
KW   Inhibitor; eukaryotic; potassium channel; TRK1; TRK2; TOK1;
KW   activator; ds.
XX
OS   Homo sapiens.
XX
PN   WO200151519-A2.
XX
PD   19-JUL-2001.
XX
PF   05-JAN-2001; 2001WO-EP00055.
XX
PR   11-JAN-2000; 2000DE-1000651.
XX
PA   (AVET ) AVENTIS PHARMA DEUT GMBH.
XX
PI   Leberer E,  Leeuw T,  Ritscher A;
XX
DR   WPI; 2001-442137/47.
XX
PT   Identifying inhibitors and activators of eukaryotic potassium channels,
PT   for use as pharmaceuticals, comprises using yeast cells that express
PT   heterologous, but no endogenous, potassium channels  -
XX
PS   Disclosure; Page 46; 78pp; German.
XX
CC   This sequence represents a novel method for identifying inhibitors or
CC   activators (A) of a eukaryotic potassium channel (KC) by applying a test
CC   compound to a mutant Saccharomyces cerevisiae cell in which: (i) the
CC   three endogenous KC (TRK1, TRK2 and TOK1) are not expressed; but (ii) a
CC   eukaryotic KC is expressed heterologously, where the effect of the
CC   compound on the eukaryotic KC is then determined. The method is used to
CC   identify inhibitors or activators (A) of a eukaryotic potassium channel.
CC   (A) are potentially useful as pharmaceuticals. The method is easily
CC   automated for parallel processing of many samples, using either different
CC   concentrations of test compounds and/or different levels of heterologous
CC   gene expression. It allows identification of compounds that inhibit human
CC   KC selectively. This sequence represents the human IRK1 encoding DNA
CC   described in the method of the invention.
XX
SQ   Sequence 1284 BP; 345 A; 269 C; 322 G; 348 T; 0 other;


alignment_scores:
           Quality:  829.00              Length:    327
             Ratio:  3.264                Gaps:      5
 Percent Similarity:  77.676   Percent Identity: 51.376

alignment_block:
 US-09-623-304A-1 x AAH21453   ..

 Align seg 1/1  to: AAH21453  from: 1  to: 1284

      29 LysArgArgAlaArgArgArgLeuLeuHisLysAspGlySerCysAsnVa 45
         ::::::::::::|||   |||::::::   |||||||||   ||||||||
     118 CGGCAACAGTGTAGGAGCCGCTTTGTGAAGAAAGATGGCCACTGTAATGT 167

      45 lTyrPheLysHisIlePheGlyGluTrpGlySer...TyrValValAspI 61
         |   |||   ::::::   ||||||   |||:::   |||::::::||||
     168 TCAGTTCATCAACGTT...GGGGAAAAGGGACAACGGTACCTTGCTGACA 214

      61 lePheThrThrLeuValAspThrLysTrpArgHisMetPheValIlePhe 77
         ||||||||||||   ||||||   :::||||||   |||:::||||||||||
     215 TTTTTACTACGTGTGTGGACATTCGCTGGCGGTGGATGCTGGTTATCTTT 264

      78 SerLeuSerTyrIleLeuSerTrpLeuIlePheGlySerValPheTrpLe 94
         |||::::::::::||||||||||||:::||||||   ||||||||||
     265 TGCCTAGCTTTTGTTCTCTCGTGGCTGTTTTTTGGCTGTGTGTTTTGGCT 314

      94 uIleAlaPheHisHisGlyAspLeuLeuAsnAspProAspIleThrProC 111
         ||||||||:::   ||||||||||||      :::   :::         |
     315 GATAGCTTTGCTCCATGGAGATCTGGATGCATCTAAGGAGAGCAAAGCCT 364

     111 ysValAspAsnValHisSerPheThrGlyAlaPheLeuPheSerLeuGlu 127
         ||||:::::::|||:::|||||||||:::|||||||||||||||||:::|||
     365 GTGTGTCTGAGGTCAACAGCTTCACAGCTGCCTTTCTTTTCTCCATTGAG 414

     128 ThrGlnThrThrIleGlyTyrGlyTyrArgCysValThrGluGluCysSe 144
         ||||||||||||||||||||||:::|||||||||||||:::||||||
     415 ACCCAGACAACCATCGGCTATGGGTTCCGATGTGTCACGGATGAATGCCC 464

     144 rValAlaValLeuMetValIleLeuGlnSerIleLeuSerCysIleIleA 161
          :::||||||:::||||||:::::|||||||||:::::|||||||||:
     465 GATTGCGGTGTTCATGGTTGTGTTCCAGTCAATTGTGGGCTGCATTATTG 514

     161 snThrPheIleIleGlyAlaAlaLeuAlaLysMetAlaThrAlaArgLys 177
         :::::|||||||||||||||:::::|||||||||||       :::|||
     515 ATGCTTTTATCATTGGTGCCGTCATGGCAAAGATGGCAAAGCCAAAGAAA 564

     178 ArgAlaGlnThrIleArgPheSerTyrPheAlaLeuIleGlyMetArgAs 194
         |||   :::|||:::   ||||||:::   |||:::|||:::||||||||
     565 AGAAATGAGACTCTTGTCTTCAGTCACAATGCTGTGATTGCCATGAGAGA 614

     194 pGlyLysLeuCysLeuMetTrpArgIleGlyAspPheArgProAsnHisV 211
         ||||||||||||||||||||||:::|||:::::|||   :::|||:
     615 TGGCAAGCTGTGTTTGATGTGGCGAGTAGGCAACCTTCGGAAAAGCCACT 664
```

```
     211 alValGluGlyThrValArgAlaGlnLeuLeuArgTyrThrGluAspSer 227
         ::||||||:::   ||||||||||||||||||:::            |||
     665 TGGTAGAAGCTCATGTTCGAGCCCAGCTCCTCAAATCCAGAATTACTTCT 714

     228 GluGlyArgMetThrMetAlaPheLysAspLeuLysLeuValAsn..... 242
         |||||||:::            :::      |||      ::::::
     715 GAAGGGGAA............TACATCCCCTTGGATCAAATAGACATCAA 752

     243 .....................AspGlnIleIleLeuValThrProValT 252
                              |||:::|||:::|||||||:::|||:::|
     753 TGTTGGCTTTGACAGTGGAATTGACCGTATATTTCTGGTATCCCCAATCA 802

     252 hrIleValHisGluIleAspHisGluSerProLeuTyrAlaLeuAspArg 268
         ||||||||||||||||||||:::::||||||||||||   |||:::::::
     803 CTATTGTCCATGAAATAGATGAAGATAGTCCTTTATATGATTTGAGCAAG 852

     269 LysAlaValAlaLysAspAsnPheGluIleLeuValThrPheIleTyrTh 285
         :::   :::   :::   :::||||||||||:::|||   :::
     853 CAGGACATTGATAATGCAGACTTTGAAATTGTTGTGATACTAGAAGGCAT 902

     285 rGlyAspSerThrGlyThrSerHisGlnSerArgSerSerTyrValProA 302
         ::::::|||:::   :::   |||   ||||||||||||:::   :
     903 GGTGGAAGCCACTGCCATGACAACACAGTGTCGTAGTTCTTATTTGGCCA 952

     302 rg***IleLeuTrpGlyHisArgPheAsnAspValLeuGluValLysArg 318
         ::   ||||||||||||||||||:::::   ||||||      ::::::
     953 ACGAGATCCTTTGGGGCCACCGCTATGAGCCAGTGCTCTTTGAGGAGAAG 1002

     319 LysTyrTyrLysValAsnCysLeuGlnPheGluGlySerValGluVal.. 334
           ||||||||||||:::      :::|||:::   :::   ||||||
    1003 CACTACTATAAAGTGGACTATTCGAGGTTTCATAAGACTTACGAAGTACC 1052

     335 .TyrAlaProPheCysSerAlaLysGlnLeu 344
           :::|||:::|||||||||:::::::|||
    1053 CAACACTCCCCTTTGTAGTGCCAGAGACTTA 1083
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seq_name: /SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA2001A.DAT:ABA35969

seq_documentation_block:

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ID   ABA35969 standard; DNA; 1310 BP.
XX
AC   ABA35969;
XX
DT   23-JAN-2002  (first entry)
XX
DE   Probe #14435 for gene expression analysis in human heart cell sample.
XX
KW   Human; gene expression; heart; microarray; vascular system; probe;
KW   cardiovascular disease; hypertension; cardiac arrhythmia;
KW   congenital heart disease; ss.
XX
OS   Homo sapiens.
XX
PN   WO200157274-A2.
XX
PD   09-AUG-2001.
XX
PF   30-JAN-2001; 2001WO-US00666.
XX
PR   04-FEB-2000; 2000US-0180312.
PR   26-MAY-2000; 2000US-0207456.
PR   30-JUN-2000; 2000US-0608408.
PR   03-AUG-2000; 2000US-0632366.
PR   21-SEP-2000; 2000US-0234687.
PR   27-SEP-2000; 2000US-0236359.
PR   04-OCT-2000; 2000GB-0024263.
XX
PA   (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI   Penn SG,  Hanzel DK,  Chen W,  Rank DR;
XX
DR   WPI; 2001-488899/53.
XX
PT   Single exon nucleic acid probes for analyzing gene expression in human
PT   hearts -
XX
PS   Claim 4; SEQ ID No 14435; 530pp; English.
XX
CC   The present invention relates to single exon nucleic acid probes for
CC   measuring human gene expression in a sample derived from human heart. The
CC   present sequence is one such probe. The probes may be used for
CC   predicting, measuring and displaying gene expression in samples derived
CC   from the human heart via microarrays. By measuring gene expression, the
CC   probes are useful for predicting, diagnosing, grading, staging,
CC   monitoring and prognosing diseases of the human heart and vascular system
CC   e.g. cardiovascular disease, hypertension, cardiac arrhythmias and
CC   congenital heart disease.
CC   Note: The sequence data for this patent did not form part of the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 1310 BP; 354 A; 302 C; 336 G; 318 T; 0 other;
```

alignment_scores:

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           Quality:  827.00              Length:    327
             Ratio:  3.256                 Gaps:      5
 Percent Similarity:  77.676   Percent Identity: 51.376
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alignment_block:

US-09-623-304A-1 x ABA35969 ..

Align seg 1/1 to: ABA35969 from: 1 to: 1310

```
      29 LysArgArgAlaArgArgArgLeuLeuHisLysAspGlySerCysAsnVa 45
         :::::::::::|||   |||::::::   |||||||||   ||||||||
     144 CGACAACAGTGCAGGAGCCGCTTTGTGAAGAAAGATGGCCACTGTAATGT 193

      45 lTyrPheLysHisIlePheGlyGluTrpGlySer...TyrValValAspI 61
         |   |||   ::::::   ||||||   |||:::   |||::::::||||
     194 TCAGTTCATCAATGTG...GGTGAGAAGGGGCAACGGTACCTCGCAGACA 240

      61 lePheThrThrLeuValAspThrLysTrpArgHisMetPheValIlePhe 77
         ||||||||||   ||||||   :::||||||   |||:::|||||||||
     241 TCTTCACCACGTGTGTGGACATTCGCTGGCGGTGGATGCTGGTTATCTTC 290

      78 SerLeuSerTyrIleLeuSerTrpLeuIlePheGlySerValPheTrpLe 94
            |||::::::::::|||||||||||||:::||||||   ||||||||||
     291 TGCCTGGCTTTCGTCCTGTCATGGCTGTTTTTTGGCTGTGTGTTTTGGTT 340

      94 uIleAlaPheHisHisGlyAspLeuLeuAsnAspProAspIleThrProC 111
         |||||||:::   ||||||||||||      :::   :::          |
     341 GATAGCTCTGCTCCATGGGGACCTGGATGCATCCAAAGAGGGCAAAGCTT 390

     111 ysValAspAsnValHisSerPheThrGlyAlaPheLeuPheSerLeuGlu 127
         |||||:::::::|||:::|||||||||:::|||||||||||||||:::|||
     391 GTGTGTCCGAGGTCAACAGCTTCACGGCTGCCTTCCTCTTCTCCATTGAG 440

     128 ThrGlnThrThrIleGlyTyrGlyTyrArgCysValThrGluGluCysSe 144
         ||||||||||||||||||||||||:::||||||||||||:::||||||
     441 ACCCAGACAACCATAGGCTATGGTTTCAGATGTGTCACGGATGAATGCCC 490

     144 rValAlaValLeuMetValIleLeuGlnSerIleLeuSerCysIleIleA 161
          :::|||||||:::||||||:::::::||||||||:::::::||||||||:
     491 AATTGCTGTTTTCATGGTGGTGTTCCAGTCAATCGTGGGCTGCATCATCG 540

     161 snThrPheIleIleGlyAlaAlaLeuAlaLysMetAlaThrAlaArgLys 177
         :::::|||||||||||||||:::::|||||||||||      :::|||
     541 ATGCTTTCATCATTGGCGCAGTCATGGCCAAGATGGCAAAGCCAAAGAAG 590

     178 ArgAlaGlnThrIleArgPheSerTyrPheAlaLeuIleGlyMetArgAs 194
         |||   :::|||:::   |||||||:::   |||:::|||:::||||||||
     591 AGAAACGAGACTCTTGTCTTCAGTCACAATGCCGTGATTGCCATGAGAGA 640

     194 pGlyLysLeuCysLeuMetTrpArgIleGlyAspPheArgProAsnHisV 211
```

```
      |||||||||||||||||||||||||:::|||::::::|||   :::|||:
    641 CGGCAAGCTGTGTTTGATGTGGCGAGTGGGCAATCTTCGGAAAAGCCACT 690

    211 alValGluGlyThrValArgAlaGlnLeuLeuArgTyrThrGluAspSer 227
        ::|||||:::   |||||||||||||||||:::           |||
    691 TGGTGGAAGCTCATGTTCGAGCACAGCTCCTCAAATCCAGAATTACTTCT 740

    228 GluGlyArgMetThrMetAlaPheLysAspLeuLysLeuValAsn..... 242
        ||||||:::          :::     |||     ::::::
    741 GAAGGGGAG...........TATATCCCTCTGGATCAAATAGACATCAA 778

    243 ..................AspGlnIleIleLeuValThrProValT 252
                           |||:::|||:::|||||||:::|||:::|
    779 TGTTGGGTTTGACAGTGGAATCGATCGTATATTTCTGGTGTCCCCAATCA 828

    252 hrIleValHisGluIleAspHisGluSerProLeuTyrAlaLeuAspArg 268
        ||||||||||||||||||||:::::|||||||||||||   |||::::::
    829 CTATAGTCCATGAAATAGATGAAGACAGTCCTTTATATGATTTGAGTAAA 878

    269 LysAlaValAlaLysAspAsnPheGluIleLeuValThrPheIleTyrTh 285
        :::   :::   :::   :::||||||||||:::|||   :::
    879 CAGGACATTGACAACGCAGACTTTGAAATCGTGGTCATACTGGAAGGCAT 928

    285 rGlyAspSerThrGlyThrSerHisGlnSerArgSerSerTyrValProA 302
          ::::::|||:::   :::   |||   ||||||||||||:::   :
    929 GGTGGAAGCCACTGCCATGACGACACAGTGCCGTAGCTCTTATCTAGCAA 978

    302 rg***IleLeuTrpGlyHisArgPheAsnAspValLeuGluValLysArg 318
        ::   ||||||||||||||||||:::::   ||||||      ::::::
    979 ATGAAATCCTGTGGGGCCACCGCTATGAGCCTGTGCTCTTTGAAGAGAAG 1028

    319 LysTyrTyrLysValAsnCysLeuGlnPheGluGlySerValGluVal.. 334
           ||||||||||||:::      :::|||:::   :::   ||||||
   1029 CACTACTACAAAGTGGACTATTCCAGGTTCCACAAAACTTACGAAGTCCC 1078

    335 .TyrAlaProPheCysSerAlaLysGlnLeu 344
          :::|||:::|||||||||:::::::|||
   1079 CAACACTCCCCTTTGTAGTGCCAGAGACTTA 1109
```

seq_name: /SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA2001A.DAT:AAK17341

seq_documentation_block:

```
ID   AAK17341 standard; DNA; 1310 BP.
XX
AC   AAK17341;
XX
DT   05-NOV-2001  (first entry)
XX
DE   Human brain expressed single exon probe SEQ ID NO: 17332.
XX
KW   Human; brain expressed exon; gene expression analysis; probe;
KW   microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;
KW   epilepsy; cancer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200157275-A2.
XX
PD   09-AUG-2001.
XX
PF   30-JAN-2001; 2001WO-US00667.
XX
PR   04-FEB-2000; 2000US-0180312.
PR   26-MAY-2000; 2000US-0207456.
PR   30-JUN-2000; 2000US-0608408.
PR   03-AUG-2000; 2000US-0632366.
PR   21-SEP-2000; 2000US-0234687.
PR   27-SEP-2000; 2000US-0236359.
PR   04-OCT-2000; 2000GB-0024263.
XX
PA   (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI   Penn SG,  Hanzel DK,  Chen W,  Rank DR;
XX
DR   WPI; 2001-483446/52.
XX
PT   Single exon nucleic acid probes for analyzing gene expression in human
PT   brains -
XX
PS   Example 4; SEQ ID NO: 17332; 650pp + Sequence Listing; English.
XX
CC   The present invention provides a number of single exon nucleic acid
CC   probes which are derived from genomic sequences expressed in the human
CC   brain. They can be used to measure gene expression in brain cell samples,
CC   which may enable the diagnosis and improved treatment of nervous system
CC   diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
CC   epilepsy and cancers. The present sequence is one of the probes of the
CC   invention.
XX
SQ   Sequence 1310 BP; 354 A; 302 C; 336 G; 318 T; 0 other;
```

alignment_scores:

```
            Quality:  827.00              Length:    327
              Ratio:  3.256                 Gaps:      5
 Percent Similarity:  77.676   Percent Identity: 51.376
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alignment_block:

US-09-623-304A-1 x AAK17341 ..

Align seg 1/1 to: AAK17341 from: 1 to: 1310

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     29 LysArgArgAlaArgArgArgLeuLeuHisLysAspGlySerCysAsnVa 45
        :::::::::::::|||   |||::::::   |||||||||   ||||||||
    144 CGACAACAGTGCAGGAGCCGCTTTGTGAAGAAAGATGGCCACTGTAATGT 193

     45 lTyrPheLysHisIlePheGlyGluTrpGlySer...TyrValValAspI 61
        |   |||   ::::::   ||||||   |||:::   |||:::::::|||
    194 TCAGTTCATCAATGTG...GGTGAGAAGGGGCAACGGTACCTCGCAGACA 240

     61 lePheThrThrLeuValAspThrLysTrpArgHisMetPheValIlePhe 77
        ||||||||||   ||||||   :::||||||   |||:::|||||||||
    241 TCTTCACCACGTGTGTGGACATTCGCTGGCGGTGGATGCTGGTTATCTTC 290

     78 SerLeuSerTyrIleLeuSerTrpLeuIlePheGlySerValPheTrpLe 94
          |||:::::::::|||||||||||||:::||||||   ||||||||||
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XX
PA   (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI   Penn SG,  Hanzel DK,  Chen W,  Rank DR;
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DR   WPI; 2001-488897/53.
XX
PT   Human genome-derived single exon nucleic acid probes useful for
PT   analyzing gene expression in human placenta -
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PS   Claim 25; SEQ ID No 17900; 654pp; English.
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CC   The present invention relates to single exon nucleic acid probes (SENP).
CC   The present sequence is one such probe. The probes are useful for
CC   producing a microarray for predicting, measuring and displaying gene
CC   expression in samples derived from human placenta. The probes are useful
CC   for antenatal diagnosis of human genetic disorders.
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About: Results were produced by the GenCore software, version 4.5,
       Copyright (c) 1993-2000 Compugen Ltd.

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;    APPLICANT:  Jan, Lily Y.
;    APPLICANT:  Jan, Yuh Nung
;    APPLICANT:  Kubo, Yoshihiro
;    APPLICANT:  Reuveny, Eitan
;    APPLICANT:  Slesinger, Paul A.
;    TITLE OF INVENTION:  Cloning of Mammalian Inward Rectifier
;    TITLE OF INVENTION:  Potassium Channel cDNAs
;    NUMBER OF SEQUENCES:  26
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Flehr, Hohbach, Test, Albritton & Herbert
;      STREET:  Four Embarcadero Center, Suite 3400
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  United States
;      ZIP:  94111-4187
;    COMPUTER READABLE FORM:
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;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
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;      APPLICATION NUMBER:  US/08/461,690B
;      FILING DATE:  05-JUN-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/103,445
;      FILING DATE:  06-AUG-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Dreger, Walter H.
;      REGISTRATION NUMBER:  24,190
;      REFERENCE/DOCKET NUMBER:  A-58619-1/WHD/JPB
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 781-1989
;      TELEFAX:  (415) 398-3249
;      TELEX:  910 277299
;  INFORMATION FOR SEQ ID NO:  1:
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     902 AGAAATGAGACTCTTGTCTTCAGTCACAATGCTGTGATTGCCATGAGGGA 951

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     952 TGGCAAACTCTGCTTGATGTGGAGAGTGGGTAACCTTCGAAAGAGCCACC 1001

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seq_documentation_block:
; Sequence 1, Application US/08103445
; Patent No. 5492825
;  GENERAL INFORMATION:
;    APPLICANT:  Jan, Lily Y.
;    APPLICANT:  Jan, Yuh Nung
;    APPLICANT:  Kubo, Yoshihiro
;    APPLICANT:  Reuveny, Eitan
;    APPLICANT:  Slesinger, Paul A.
;    TITLE OF INVENTION:  Cloning of Mammalian Inward Rectifier
;    TITLE OF INVENTION:  Potassium Channel cDNAs
;    NUMBER OF SEQUENCES:  26
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Flehr, Hohbach, Test, Albritton & Herbert
;      STREET:  4 Embarcadero Center, Suite 3400
;      CITY:  San Francisco,
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94111-4187
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/103,445
;      FILING DATE:  06-AUG-1993
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Dreger, Walter H.
;      REGISTRATION NUMBER:  24,190
;      REFERENCE/DOCKET NUMBER:  A-58619/WHD
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 781-1989
;      TELEFAX:  (415) 398-3249
;      TELEX:  910 277299
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2311 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  338..1624
;    FEATURE:
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;     FEATURE:
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US-08-103-445-1


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      61 lePheThrThrLeuValAspThrLysTrpArgHisMetPheValIlePhe 77
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     552 TCTTTACTACCTGTGTCGACATCCGCTGGAGGTGGATGCTGGTTATCTTC 601

      78 SerLeuSerTyrIleLeuSerTrpLeuIlePheGlySerValPheTrpLe 94
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     602 TGTCTTGCCTTCGTGCTCTCCTGGCTGTTCTTTGGCTGTGTGTTTTGGTT 651

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     652 GATAGCCCTGCTCCATGGGGATCTAGATACTTCTAAAGTGAGCAAAGCAT 701

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seq_documentation_block:
; Sequence 5, Application US/08614801A
; Patent No. 5744324
;  GENERAL INFORMATION:
;    APPLICANT:  Lester, Henry A.
;    APPLICANT:  Davidson, No. 5744324man
;    APPLICANT:  Kofuji, Paulo
;    TITLE OF INVENTION:  INWARD RECTIFIER, G-PROTEIN ACTIVATED,
;    TITLE OF INVENTION:  MAMMALIAN, POTASSIUM CHANNELS AND USES THEREOF
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Flehr, Hohbach, Test, Albritton & Herbert
;      STREET:  Four Embarcadero Center, Suite 3400
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  United States
;      ZIP:  94111-4187
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/614,801A
;      FILING DATE:  07-MAR-1996
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/066,371
;      FILING DATE:  21-MAR-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Trecartin, Richard F.
;      REGISTRATION NUMBER:  31,801
;      REFERENCE/DOCKET NUMBER:  A-63098/RFT
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 781-1989
;      TELEFAX:  (415) 398-3249
;      TELEX:  910 277299
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;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2301 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  unknown
;      TOPOLOGY:  unknown
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  308..1435
US-08-614-801A-5


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; Patent No. 5744324
;  GENERAL INFORMATION:
;    APPLICANT:  Lester, Henry A.
;    APPLICANT:  Davidson, No. 5744324man
;    APPLICANT:  Kofuji, Paulo
;    TITLE OF INVENTION:  INWARD RECTIFIER, G-PROTEIN ACTIVATED,
;    TITLE OF INVENTION:  MAMMALIAN, POTASSIUM CHANNELS AND USES THEREOF
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Flehr, Hohbach, Test, Albritton & Herbert
;      STREET:  Four Embarcadero Center, Suite 3400
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  United States
;      ZIP:  94111-4187
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/614,801A
;      FILING DATE:  07-MAR-1996
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/066,371
;      FILING DATE:  21-MAR-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Trecartin, Richard F.
;      REGISTRATION NUMBER:  31,801
;      REFERENCE/DOCKET NUMBER:  A-63098/RFT
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 781-1989
;      TELEFAX:  (415) 398-3249
;      TELEX:  910 277299
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1978 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  unknown
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;       TOPOLOGY:  unknown
;     MOLECULE TYPE:  DNA (genomic)
;     FEATURE:
;       NAME/KEY:  CDS
;       LOCATION:  488..1729
US-08-614-801A-3


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              Ratio:  2.854                Gaps:      5
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    1361 TGGGAGATCTCCAAAGCGCAGCTGCCTAAAGAGGAACTGGAGATTGTGGT 1410

     280 lThrPheIleTyrThrGlyAspSerThrGlyThrSerHisGlnSerArgS 297
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     297 erSerTyrValProArg***IleLeuTrpGlyHisArgPheAsnAspVal 313
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    1461 GCTCCTACATCACCAGTGAGATCTTGTGGGGTTACCGGTTCACACCTGTC 1510

     314 LeuGluValLysArgLysTyrTyrLysValAsnCysLeuGlnPheGluGl 330
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seq_name: /cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-385-186-14

seq_documentation_block:
; Sequence 14, Application US/08385186
; Patent No. 5744594
;  GENERAL INFORMATION:
;    APPLICANT:  Adelman, John P
;    APPLICANT:  Ashford, Michael J
;    APPLICANT:  Bond, Chris T
;    TITLE OF INVENTION:  DNA ENCODING ATP-SENSITIVE POTASSIUM
;    TITLE OF INVENTION:  CHANNEL PROTEINS AND USES THEREOF
;    NUMBER OF SEQUENCES:  15
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend Khourie and Crew
;      STREET:  Steuart Street Tower, One Market Plaza
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  US
;      ZIP:  94105-1493
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/385,186
;      FILING DATE:  07-FEB-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/288,510
;      FILING DATE:  10-AUG-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/193,372
;      FILING DATE:  08-FEB-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Kruse, No. 5744594man J.
;      REGISTRATION NUMBER:  35,235
;      REFERENCE/DOCKET NUMBER:  14210-2-2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 543-9600
;      TELEFAX:  (415) 543-5043
;  INFORMATION FOR SEQ ID NO:  14:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1245 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
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;    HYPOTHETICAL:  NO
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  22..1242
;      OTHER INFORMATION:  /note= "Encodes a full-length or
;      OTHER INFORMATION:  nearly full-length human pancreatic beta cell
;      OTHER INFORMATION:  ATP-sensitive potassium channel protein: Seq ID.
;      OTHER INFORMATION:  15."
US-08-385-186-14


alignment_scores:
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              Ratio:  2.861                Gaps:      5
 Percent Similarity:  77.039   Percent Identity: 41.994

alignment_block:
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      94 CCAAGACACATCAGCCGAGATCGGACCAAAAGGAAAATCCAGAGGTACGT 143

      37 uHisLysAspGlySerCysAsnValTyrPheLysHisIlePheGlyGluT 54
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     144 GAGGAAAGACGGAAAGTGCAATGTTCATCACGGCAACGTG...AGGGAGA 190

      54 rpGlySerTyrValValAspIlePheThrThrLeuValAspThrLysTrp 70
                 |||:::::::||||||||||||||||||||||||||   ||||||
     191 CCTATCGCTACCTGACCGATATCTTCACCACATTAGTGGACCTGAAGTGG 240

      71 ArgHisMetPheValIlePheSerLeuSerTyrIleLeuSerTrpLeuIl 87
         |||      ::::::||||||   :::   |||   ::::::||||||::
     241 AGATTCAACCTATTGATTTTTGTCATGGTTTACACAGTGACCTGGCTCTT 290

      87 ePheGlySerValPheTrpLeuIleAlaPheHisHisGlyAspLeu.... 102
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     291 TTTTGGAATGATCTGGTGGTTGATCGCATACATACGGGGAGACATGGACC 340

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     341 ACATAGAGGACCCCTCCTGGACTCCTTGTGTTACCAACCTCAACGGGTTC 390

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     541 TTTGTAAAAATCTCTCAACCCAAGAAGAGGGCAGAGACCCTGGTCTTTTC 590

     185 rTyrPheAlaLeuIleGlyMetArgAspGlyLysLeuCysLeuMetTrpA 202
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     591 CACCCATGCAGTGATCTCCATGCGGGATGGGAAACTGTGCCTGATGTTCC 640

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     641 GGGTAGGGGACCTTAGGAATTCCCACATTGTGGAGGCTTCCATCAGAGCC 690

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seq_name: /cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-385-186-12

seq_documentation_block:
; Sequence 12, Application US/08385186
; Patent No. 5744594
;  GENERAL INFORMATION:
;    APPLICANT:  Adelman, John P
;    APPLICANT:  Ashford, Michael J
;    APPLICANT:  Bond, Chris T
;    TITLE OF INVENTION:  DNA ENCODING ATP-SENSITIVE POTASSIUM
;    TITLE OF INVENTION:  CHANNEL PROTEINS AND USES THEREOF
;    NUMBER OF SEQUENCES:  15
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend Khourie and Crew
;      STREET:  Steuart Street Tower, One Market Plaza
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  US
;      ZIP:  94105-1493
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/385,186
;      FILING DATE:  07-FEB-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/288,510
;      FILING DATE:  10-AUG-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/193,372
;      FILING DATE:  08-FEB-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Kruse, No. 5744594man J.
;      REGISTRATION NUMBER:  35,235
;      REFERENCE/DOCKET NUMBER:  14210-2-2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 543-9600
;      TELEFAX:  (415) 543-5043
;  INFORMATION FOR SEQ ID NO:  12:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1425 base pairs
;      TYPE:  nucleic acid
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;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  cDNA
;     FEATURE:
;       NAME/KEY:  CDS
;       LOCATION:  56..1330
;     FEATURE:
;       NAME/KEY:  misc_feature
;       LOCATION:  1..1425
;       OTHER INFORMATION:  /note= "Encodes rat pancreatic beta
;       OTHER INFORMATION:  cell ATP-sensitive potassium channel protein."
US-08-385-186-12

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 Percent Similarity:  76.435   Percent Identity: 41.994

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      54 rpGlySerTyrValValAspIlePheThrThrLeuValAspThrLysTrp 70
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seq_documentation_block:
; Sequence 1, Application US/08385186
; Patent No. 5744594
;  GENERAL INFORMATION:
;    APPLICANT:  Adelman, John P
;    APPLICANT:  Ashford, Michael J
;    APPLICANT:  Bond, Chris T
;    TITLE OF INVENTION:  DNA ENCODING ATP-SENSITIVE POTASSIUM
;    TITLE OF INVENTION:  CHANNEL PROTEINS AND USES THEREOF
;    NUMBER OF SEQUENCES:  15
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend Khourie and Crew
;      STREET:  Steuart Street Tower, One Market Plaza
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  US
;      ZIP:  94105-1493
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/385,186
;      FILING DATE:  07-FEB-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/288,510
;      FILING DATE:  10-AUG-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/193,372
;      FILING DATE:  08-FEB-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Kruse, No. 5744594man J.
;      REGISTRATION NUMBER:  35,235
;      REFERENCE/DOCKET NUMBER:  14210-2-2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 543-9600
;      TELEFAX:  (415) 543-5043
;  INFORMATION FOR SEQ ID NO:  1:
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;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1260 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    HYPOTHETICAL:  NO
;    ORIGINAL SOURCE:
;      ORGANISM:  Homo sapien
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..1257
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  1..1260
;      OTHER INFORMATION:  /note= "cDNA encoding human heart
;      OTHER INFORMATION:  ATP-sensitive potassium channel protein."
US-08-385-186-1


alignment_scores:
            Quality:  716.50              Length:    399
              Ratio:  2.559                 Gaps:      9
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alignment_block:
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     954 CCGGAGCTCCTACATGGATACAGAGGTGCTCTGGGGCCACCGATTCACAC 1003

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seq_documentation_block:
; Sequence 3, Application US/08385186
; Patent No. 5744594
;  GENERAL INFORMATION:
;    APPLICANT:  Adelman, John P
;    APPLICANT:  Ashford, Michael J
;    APPLICANT:  Bond, Chris T
;    TITLE OF INVENTION:  DNA ENCODING ATP-SENSITIVE POTASSIUM
;    TITLE OF INVENTION:  CHANNEL PROTEINS AND USES THEREOF
;    NUMBER OF SEQUENCES:  15
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend Khourie and Crew
;      STREET:  Steuart Street Tower, One Market Plaza
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  US
;      ZIP:  94105-1493
;    COMPUTER READABLE FORM:
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;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/385,186
;       FILING DATE:  07-FEB-1995
;       CLASSIFICATION:  435
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 08/288,510
;       FILING DATE:  10-AUG-1994
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 08/193,372
;       FILING DATE:  08-FEB-1994
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Kruse, No. 5744594man J.
;       REGISTRATION NUMBER:  35,235
;       REFERENCE/DOCKET NUMBER:  14210-2-2
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (415) 543-9600
;       TELEFAX:  (415) 543-5043
;   INFORMATION FOR SEQ ID NO:  3:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  1260 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  cDNA
;     HYPOTHETICAL:  NO
;     ORIGINAL SOURCE:
;       ORGANISM:  Rat
;     FEATURE:
;       NAME/KEY:  misc_feature
;       LOCATION:  1..1260
;       OTHER INFORMATION:  /note= "cDNA for rat heart
;       OTHER INFORMATION:  ATP-sensitive potassium channel protein."
;     FEATURE:
;       NAME/KEY:  CDS
;       LOCATION:  1..1257
;     FEATURE:
;       NAME/KEY:  primer_bind
;       LOCATION:  472..491
;       OTHER INFORMATION:  /note= "Sequence corresponding to
; Patent No. 5744594
;       OTHER INFORMATION:  Seq. I.D. No. 5744594 5."
;     FEATURE:
;       NAME/KEY:  primer_bind
;       LOCATION:  632..651
;       OTHER INFORMATION:  /note= "Sequence complementary to
; Patent No. 5744594
;       OTHER INFORMATION:  Seq. I.D. No. 5744594:6"
US-08-385-186-3


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              Ratio:  2.644                 Gaps:      6
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       7 GGTGATTCTAGGAATGCTATGAATCAAGACATGGAGATAGGAGTCACCTC 56

      21 oProGluHis..................................... 24
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      57 CCAGGACCACAAGAAGATCCCCAAACAGGCTCGGGATTACATCCCCATTG 106

      25 ................IleIleAlaGluLysArgArgAlaArgArgArg 35
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     107 CCACAGACCGCACTCGCCTGCTGCCGGAAGGCAAGAAGCCACGCCAGCGC 156

      36 LeuLeuHisLysAspGlySerCysAsnValTyrPheLysHisIlePheGl 52
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     157 TACATGGAGAAGACCGGCAAGTGTAACGTGCACCATGGCAATGTT...CA 203

      52 yGluTrpGlySerTyrValValAspIlePheThrThrLeuValAspThrL 69
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     204 GGAAACCTACCGCTACCTAAGTGACCTCTTCACCACCCTGGTGGACCTCA 253

      69 ysTrpArgHisMetPheValIlePheSerLeuSerTyrIleLeuSerTrp 85
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     254 AATGGCGCTTCAACCTTCTGGTCTTCACCATGGTCTACACCATTACTTGG 303

      86 LeuIlePheGlySerValPheTrpLeuIleAlaPheHisHisGlyAspLe 102
         |||:::||||||   ::::::|||||||||||||:::   :::|||||||||
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     102 u......LeuAsnAspProAspIleThrProCysValAspAsnValHisS 117
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     354 GGACCACGTGGGTGACCAAGAGTGCATCCCTTGTGTTGAAAACCTTAGTG 403

     117 erPheThrGlyAlaPheLeuPheSerLeuGluThrGlnThrThrIleGly 133
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     404 GCTTTGTGTCTGCTTTCCTGTTCTCCATTGAGACAGAAACAACCATTGGG 453

     134 TyrGlyTyrArgCysValThrGluGluCysSerValAlaValLeuMetVa 150
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     604 TTCTCCAACAATGCTGTCATCTCCATGCGGGATGAGAAGCTATGCCTCAT 653

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     654 GTTCCGGGTAGGGGACCTCCGAAACTCCCATATCGTGGAGGCCTTCATCC 703

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     704 GCGCCAAGCTTATCAAGTCCCGGCAGACCAAAGAAGGGGAATTCATCCCC 753

     233 MetAlaPheLysAspLeuLysLeu............ValAsnAspGlnIl 245
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     754 TTGAACCAGACCGACATTAACGTGGGCTTTGACACTGGTGACGACCGCCT 803

     245 eIleLeuValThrProValThrIleValHisGluIleAspHisGluSerP 262
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     804 CTTCCTGGTGTCCCCCCTCTTCATCTCCCATGAGATCAATGAGAAGAGCC 853

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seq_name: /cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-385-186-8

seq_documentation_block:
; Sequence 8, Application US/08385186
; Patent No. 5744594
;  GENERAL INFORMATION:
;    APPLICANT:  Adelman, John P
;    APPLICANT:  Ashford, Michael J
;    APPLICANT:  Bond, Chris T
;    TITLE OF INVENTION:  DNA ENCODING ATP-SENSITIVE POTASSIUM
;    TITLE OF INVENTION:  CHANNEL PROTEINS AND USES THEREOF
;    NUMBER OF SEQUENCES:  15
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend Khourie and Crew
;      STREET:  Steuart Street Tower, One Market Plaza
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  US
;      ZIP:  94105-1493
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/385,186
;      FILING DATE:  07-FEB-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/288,510
;      FILING DATE:  10-AUG-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/193,372
;      FILING DATE:  08-FEB-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Kruse, No. 5744594man J.
;      REGISTRATION NUMBER:  35,235
;      REFERENCE/DOCKET NUMBER:  14210-2-2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 543-9600
;      TELEFAX:  (415) 543-5043
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1095 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    HYPOTHETICAL:  NO
;    ORIGINAL SOURCE:
;      ORGANISM:  Rat
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  1..1095
;      OTHER INFORMATION:  /note= "Sequence of cDNA clone
; Patent No. 5744594
;      OTHER INFORMATION:  encoding a portion of rat pancreatic beta-cell
;      OTHER INFORMATION:  ATP-sensitive potassium channel protein."
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  333..366
;      OTHER INFORMATION:  /note= "Sequence corresponding to
; Patent No. 5744594
;      OTHER INFORMATION:  Seq. I.D. No. 5744594:7"
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;      NAME/KEY:  CDS
;      LOCATION:  1..1092
US-08-385-186-8


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seq_documentation_block:
; Sequence 2, Application US/08614155B
; Patent No. 5919692
;  GENERAL INFORMATION:
;    APPLICANT:  Susumu SEINO et al.
;    TITLE OF INVENTION:  NOVEL UBIQUITOUS POTASSIUM-CHANNEL
;    TITLE OF INVENTION:  PROTEINS AND THEIR GENES
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  JACOBSON, PRICE, HOLMAN & STERN, PLLC
;      STREET:  400 Seventh Street, N.W.
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  U.S.A.
;      ZIP:  20004
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WordPerfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/614,155B
;      FILING DATE:  12-MAR-1996
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 264942/1995
;      FILING DATE:  18-SEP-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  PLAYER, William E.
;      REGISTRATION NUMBER:  31,409
;      REFERENCE/DOCKET NUMBER:  10890/P60281US0
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-638-6666
;      TELEFAX:  202-393-5350
;      TELEX:  RCA 248593 IDEA UR
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1275 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-614-155B-2


alignment_scores:
            Quality:  698.50              Length:    400
              Ratio:  2.559                Gaps:      7

 Percent Similarity:  68.250   Percent Identity: 38.000

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; Sequence 3, Application US/08103445
; Patent No. 5492825
;  GENERAL INFORMATION:
;    APPLICANT:  Jan, Lily Y.
;    APPLICANT:  Jan, Yuh Nung
;    APPLICANT:  Kubo, Yoshihiro
;    APPLICANT:  Reuveny, Eitan
;    APPLICANT:  Slesinger, Paul A.
;    TITLE OF INVENTION:  Cloning of Mammalian Inward Rectifier
;    TITLE OF INVENTION:  Potassium Channel cDNAs
;    NUMBER OF SEQUENCES:  26
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Flehr, Hohbach, Test, Albritton & Herbert
;      STREET:  4 Embarcadero Center, Suite 3400
;      CITY:  San Francisco,
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94111-4187
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/103,445
;      FILING DATE:  06-AUG-1993
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Dreger, Walter H.
;      REGISTRATION NUMBER:  24,190
;      REFERENCE/DOCKET NUMBER:  A-58619/WHD
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 781-1989
;      TELEFAX:  (415) 398-3249
;      TELEX:  910 277299
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1827 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
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;      OTHER INFORMATION:  /note= "Region encoding H5
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US-08-103-445-3


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              Ratio:  2.486               Gaps:      7
 Percent Similarity:  72.727   Percent Identity: 36.883

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seq_documentation_block:
; Sequence 3, Application US/08461690B
; Patent No. 5670335
;  GENERAL INFORMATION:
;    APPLICANT:  Jan, Lily Y.
;    APPLICANT:  Jan, Yuh Nung
;    APPLICANT:  Kubo, Yoshihiro
;    APPLICANT:  Reuveny, Eitan
;    APPLICANT:  Slesinger, Paul A.
;    TITLE OF INVENTION:  Cloning of Mammalian Inward Rectifier
;    TITLE OF INVENTION:  Potassium Channel cDNAs
;    NUMBER OF SEQUENCES:  26
;    CORRESPONDENCE ADDRESS:
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;      STREET:  Four Embarcadero Center, Suite 3400
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  United States
;      ZIP:  94111-4187
;    COMPUTER READABLE FORM:
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;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/461,690B
;      FILING DATE:  05-JUN-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/103,445
;      FILING DATE:  06-AUG-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Dreger, Walter H.
;      REGISTRATION NUMBER:  24,190
;      REFERENCE/DOCKET NUMBER:  A-58619-1/WHD/JPB
;    TELECOMMUNICATION INFORMATION:
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;      TELEFAX:  (415) 398-3249
;      TELEX:  910 277299
;  INFORMATION FOR SEQ ID NO:  3:
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;      LENGTH:  1827 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  59..1561
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US-08-461-690B-3


alignment_scores:
            Quality:  696.00              Length:    385
              Ratio:  2.486                 Gaps:      7
 Percent Similarity:  72.727   Percent Identity: 36.883

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; Sequence 1, Application US/08486342
; Patent No. 5728535
;  GENERAL INFORMATION:
;    APPLICANT:  Lester, Henry A.
;    APPLICANT:  Dascal, Nathan
;    APPLICANT:  Lim, Nancy F.
;    APPLICANT:  Schreibmayer, Wolfgang
;    APPLICANT:  Davidson, No. 5728535man
;    TITLE OF INVENTION:  DNA Encoding Inward Rectifier,
;    TITLE OF INVENTION:  G-Protein
;    TITLE OF INVENTION:  Activated, Mammalian, Potassium KGA Channel and
;    TITLE OF INVENTION:  Uses
;    TITLE OF INVENTION:  Thereof
;    NUMBER OF SEQUENCES:  2
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Flehr, Hohbach, Test, Albritton
;      ADDRESSEE:  & Herbert
;      STREET:  Four Embarcadero Center, Suite 3400
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  United States
;      ZIP:  94111-4187
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/486,342
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/066,371
;      FILING DATE:  21-MAR-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Trecartin, Richard F.
;      REGISTRATION NUMBER:  31,426
;      REFERENCE/DOCKET NUMBER:  A-62319/RFT
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 781-1989
;      TELEFAX:  (415) 398-3249
;      TELEX:  910 277299
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2070 base pairs
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;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
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US-08-486-342-1


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            Quality:  696.00              Length:    385
              Ratio:  2.486                 Gaps:      7
 Percent Similarity:  72.727   Percent Identity: 36.883
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;    APPLICANT:  Lester, Henry A.
;    APPLICANT:  Dascal, Nathan
;    APPLICANT:  Lim, Nancy F.
;    APPLICANT:  Schreibmayer, Wolfgang
;    APPLICANT:  Davidson, No. 5734021man
;    TITLE OF INVENTION:  DNA Encoding Inward Rectifier,
;    TITLE OF INVENTION:  G-Protein Activated, Mammalian,
;    TITLE OF INVENTION:  Potassium KGA Channel and Uses
;    TITLE OF INVENTION:  Thereof
;    NUMBER OF SEQUENCES:  2
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;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/473,092
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/066,371
;      FILING DATE:  21-MAR-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Trecartin, Richard F.
;      REGISTRATION NUMBER:  31,426
;      REFERENCE/DOCKET NUMBER:  A-62317/RFT
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 781-1989
;      TELEFAX:  (415) 398-3249
;      TELEX:  910 277299
;  INFORMATION FOR SEQ ID NO:  1:
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;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2070 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  32..1534
US-08-473-092-1


alignment_scores:
            Quality:  696.00              Length:    385
              Ratio:  2.486                Gaps:      7
 Percent Similarity:  72.727   Percent Identity: 36.883

alignment_block:
 US-09-623-304A-1 x US-08-473-092-1   ..

 Align seg 1/1  to: US-08-473-092-1  from: 1  to: 2070

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      30 rgArgAlaArgArgArgLeuLeuHisLysAspGlySerCysAsnValTyr  46
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         ||||||||||||   |||||||||      :::   ||||||   |||:
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      80 erTyrIleLeuSerTrpLeuIlePheGlySerValPheTrpLeuIleAla  96
         ::|||   ::::::||||||:::::::::|||:::::::|||:::||||||
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         ||||||||||||||||      |||:::::::::::::::   ::::::|
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seq_name: /cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-614-801A-1

seq_documentation_block:
; Sequence 1, Application US/08614801A
; Patent No. 5744324
;  GENERAL INFORMATION:
;    APPLICANT:  Lester, Henry A.
;    APPLICANT:  Davidson, No. 5744324man
;    APPLICANT:  Kofuji, Paulo
;    TITLE OF INVENTION:  INWARD RECTIFIER, G-PROTEIN ACTIVATED,
;    TITLE OF INVENTION:  MAMMALIAN, POTASSIUM CHANNELS AND USES THEREOF
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Flehr, Hohbach, Test, Albritton & Herbert
;      STREET:  Four Embarcadero Center, Suite 3400
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  United States
;      ZIP:  94111-4187
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/614,801A
;      FILING DATE:  07-MAR-1996
;      CLASSIFICATION:  435
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;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/066,371
;      FILING DATE:  21-MAR-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Trecartin, Richard F.
;      REGISTRATION NUMBER:  31,801
;      REFERENCE/DOCKET NUMBER:  A-63098/RFT
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 781-1989
;      TELEFAX:  (415) 398-3249
;      TELEX:  910 277299
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2070 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  unknown
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  DNA (genomic)
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  32..1534
US-08-614-801A-1


alignment_scores:
            Quality:  696.00              Length:    385
              Ratio:  2.486                Gaps:      7
 Percent Similarity:  72.727   Percent Identity: 36.883

alignment_block:
 US-09-623-304A-1 x US-08-614-801A-1   ..

 Align seg 1/1  to: US-08-614-801A-1  from: 1  to: 2070

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